

# JOURNAL OF CREATION



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**Exoplanets**  
*habitable or not?*

**Patrick Matthew**  
*plagiarized by Darwin*

**Improbable singularities**  
*the 'miracles' of evolution*

**Nylon-eating bacteria**

***Genetic clocks***  
confirm the biblical timeline





# JOURNAL OF CREATION

An international journal devoted to the presentation and discussion of technical aspects of the sciences such as geology, biology, astronomy, etc., and also geography, archaeology, biblical history, philosophy, etc., as they relate to the study of biblical creation and Noah's Flood.

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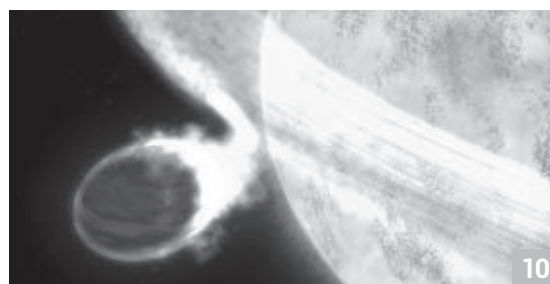
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*Glendonite as a cold-climate proxy is not reliable since it can also form in relatively warm water in the presence of methane.*



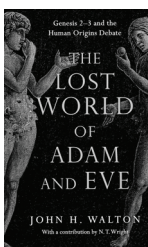
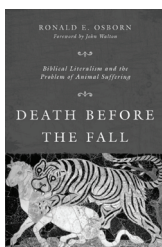
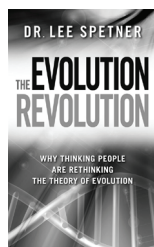
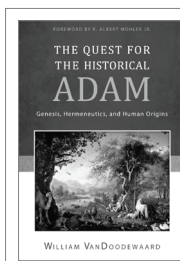
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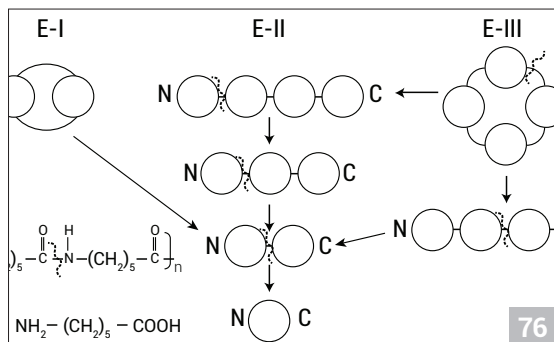


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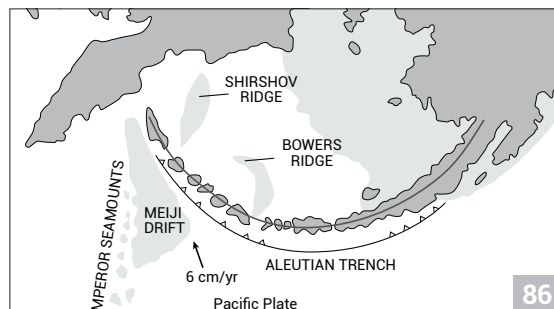
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## ABOUT US



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- » The account of origins presented in Genesis is a simple but factual presentation of actual

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- » Scripture teaches a recent origin for man and the whole creation.
- » The great Flood of Genesis was an actual historic event, worldwide (global) in its extent and effect.
- » The special creation of Adam (as one man) and Eve (as one woman) and their subsequent fall into sin, is the basis for the necessity of salvation for mankind (and thus for the Gospel of Jesus Christ).
- » The scientific aspects of creation are important, but are secondary in importance to the proclamation of the Gospel of Jesus Christ as Sovereign, Creator, Redeemer and Judge.

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# Empirical genetic clocks give biblical timelines

Jeffrey P. Tomkins

The idea of an evolutionary molecular genetic clock has significantly impacted and influenced modern biology. The technique employs biological sequence comparisons between taxa to estimate rates of evolution and is routinely calibrated with deep-time estimates taken from paleontology. In addition to this evolutionary bias, the following problems also plague its use:

- 1) different genes/sequences give widely different evolutionary rates,
- 2) different taxa exhibit different rates for homologous sequences, and
- 3) divergence dates commonly disagree with paleontology despite being calibrated by it.

Furthermore, because the molecular clock idea is directly tied to the neutral model theory of evolution, recent discoveries in full codon utility and pervasive genome-wide biochemical functionality utterly negate its foundational premises.<sup>1</sup>

What would happen if the assumption of evolution and deep time were not used to calibrate the molecular clock models? Would DNA sequence variation provide usable information to help test creationist predictions about origins? Interestingly, we have a variety of cases from both secular scientists and studies done by creationist researchers where DNA clocks were measured empirically within single taxa and without deep-time calibrations and only yielded ages of 5 to 10 thousand years, not millions. Each of these different test cases will be discussed in turn below, but first let us visit the idea of genetic entropy which is closely connected.

## Genomic entropy and genetic clocks

When mutational events occur during meiosis, they can be inherited and passed on to the next generation and when these are empirically measured within a pedigree, an estimate of the mutation rate can be achieved. In fact, scientists have actually measured this rate in the genome of humans in multiple studies and found it to be between 75 and 175 mutations per generation.<sup>2–9</sup> Using this known data about mutation rates, a variety of research groups have been able to model the accumulation of mutations in the human genome over time using complex computer simulations incorporating the standard restraints of population genetics theory.<sup>10–16</sup> They found that over 90% of deleterious mutations fail to be selected away even with intense natural selection. Because of this, the buildup of mutations would eventually reach a critical level and become so severe that humans would eventually go extinct at a point called *error castastrophe*.<sup>17,18</sup> This process of genome degradation over time and successive generations is called *genetic entropy*.<sup>17,18</sup> And remarkably, the process of human genome degradation is closely mirrored by the biblically documented trend of declining human lifespan, particularly in the last approximately 4,300 years since the Flood.<sup>15,18–20</sup> In addition to these extensive simulation studies, largely performed by intelligent design theorists, prominent evolutionists have also shown that the problem of mutation accumulation in the human genome is accompanied by the inability of selection to alleviate it.<sup>5,21</sup>

After the experimental results of genetic entropy in the human genome via computational simulation were published in multiple papers (cited above), their conclusions were spectacularly confirmed by two high-profile genetic studies based on empirical data that essentially

provided the same results, and also within a timeframe that paralleled biblical events.<sup>5,6</sup> Both secular studies involved sequencing the protein-coding regions (exons) of the human genome, called the exome.<sup>22,23</sup> The projects examined the preponderance of rare single nucleotide variants that occur in human exomes—one study analyzed 2,440 individuals and the other 6,515. Over 80% of the single nucleotide variants in protein-coding exons were considered to be deleterious or harmful (associated with heritable disease) and researchers attributed the unexpected presence of these harmful mutations to ‘weak purifying selection’. This essentially means that the alleged ability of natural selection to remove these harmful variants from human populations was powerless to do so, a finding also observed in the computer simulation models discussed above.<sup>11,14–16</sup>

A major analytical benefit of this type of rare variant data in the exome is due to the fact that protein-coding regions are less tolerant of mutation than other parts of the genome, providing more reliable historical genetic information about human populations. In addition, this type of data can be conveniently integrated into demographic models over known historical time and geographical space. When the researchers did this, they discovered a very recent massive burst of human genetic diversification, primarily associated with genetic entropy. One of the research papers stated: “The maximum likelihood time for accelerated growth was 5,115 years ago.”<sup>22</sup> The other paper uncovered a similar timeline, which places the beginning of human genetic diversification close to the Genesis Flood and subsequent dispersion of people groups at the Tower of Babel. Importantly, this recent explosion of rare genetic variants clearly associated with genetic entropy also follows the same pattern of human life expectancy

rapidly declining after the Flood as mentioned above.<sup>18,20</sup>

### Mitochondrial DNA variability and genetic clocks

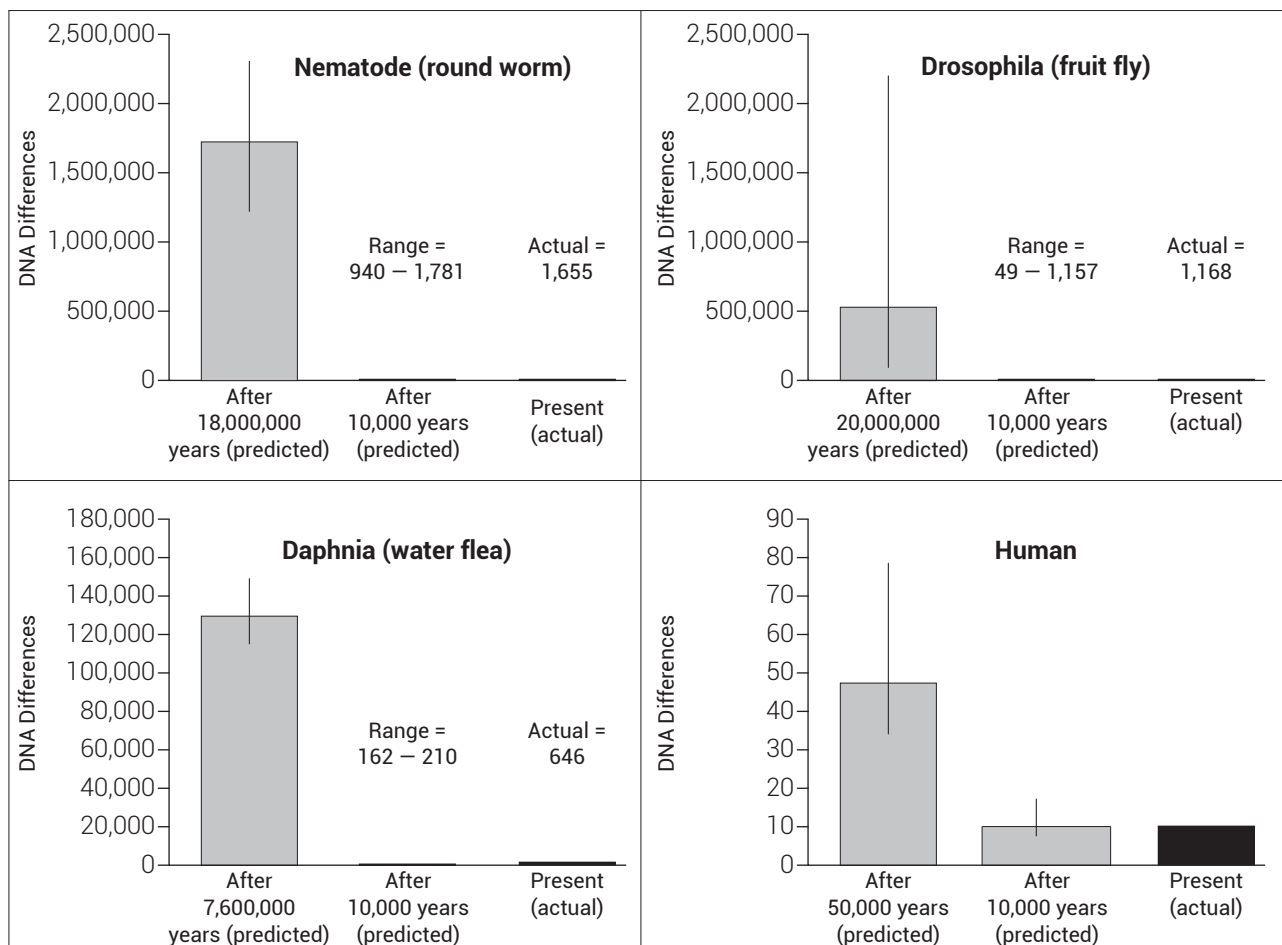
One other important realm of molecular clock research demonstrating a recent creation comes from creation scientist Nathaniel Jeanson, who has been examining mutation rates in mitochondrial genomes.<sup>24</sup> The mitochondrial DNA molecule is typically inherited maternally and its mutation rates can accurately be measured in pedigrees to produce a lineage-specific clock. When these clocks are also not calibrated by

evolutionary timescales, but by using the organism's generation time, a more realistic and unbiased estimate of that creature's genetic life history can be obtained. By comparing the empirical mitochondrial clock rates in fruit flies, round worms, water fleas, and humans, Jeanson demonstrated that a creation event for all of these organisms (including humans) occurred not more than 10,000 years ago (figure 1).

Creationist scientists Sanford and Carter have also conducted independent study into human mtDNA variation in which they statistically analyzed over 800 different sequences, and reconstructed a very close approximation of Eve's original

mitochondrial genome.<sup>18,25</sup> They found that "the average human being is only about 22 mutations removed from the Eve sequence although some individuals are as much as 100 mutations removed from Eve".<sup>18</sup> The most recent empirical estimate of the mutation rate in human mitochondria is about 0.5 per generation.<sup>26</sup> Based on this rate, even for the most mutated mitochondrial sequences, Sanford and Carter determined that "it would only require 200 generations (less than 6,000 years) to accumulate 100 mutations".<sup>18</sup>

Surprisingly, evolutionists were actually the first to note these biblically supportive timeframes. Buried within



**Figure 1.** Graphs showing the recent origin of mitochondrial DNA diversity. The first, second and third bars show the evolutionary predicted diversity (based on deep time), the amount predicted after only 10,000 years, and the amount actually found in the sequence, respectively. Black bars represent a 95% confidence interval. In all four cases, the empirical data fits a predicted biblical timeframe of 10,000 years or less. Data is calculated using average generation time and the empirical mutation rate. This image was created from data published in reference 16 by permission of the author.



a secular research paper in 1997, the same trends recently observed by creationists regarding human mtDNA mutation rates were first reported, but received little attention in the evolutionary community.<sup>27</sup> The authors of the paper state:

“Using our empirical rate to calibrate the mtDNA molecular clock would result in an age of the mtDNA MRCA [most recent common ancestor or the first human woman] of only ~6,500 years.”

One year later, another secular researcher remarked about this study stating:

“Regardless of the cause, evolutionists are most concerned about the effect of a faster mutation rate. For example, researchers have calculated that ‘mitochondrial Eve’—the woman whose mtDNA was ancestral to that in all living people—lived 100,000 to 200,000 years ago in Africa. *Using the new clock, she would be a mere 6000 years old* [emphasis added].”<sup>28</sup>

The article continues to note that the new findings of faster mutation rates that point to mitochondrial Eve about 6,000 years ago, have even contributed to the development of new mtDNA research guidelines used in forensic investigations adopted by the FBI. Now, over 17 years later, and using even more mtDNA data, Jeanson, Carter, and Sanford are spectacularly confirming this previous unheralded discovery.

In addition to the mtDNA data, Sanford and Carter have also analyzed the Y chromosomes of modern men which they found to be only about 300 mutations on average different than the consensus sequence of a Y chromosome Adam.<sup>18</sup> As a result, they state:

“Even if we assume a normal mutation rate for the Y chromosome (about 1 mutation per chromosome per generation), we would only need 300 generations (about six thousand years), to get 300 mutations.”

As with their previous mtDNA work, this is the most straightforward application of the DNA clock concept and provides data perfectly in accord with a biblical timeframe for the origins of man.

## Conclusion

In contrast to the flawed evolutionary paradigm of a molecular clock that assumes evolution on a grand scale and incorporates deep-time calibrations, a straightforward empirical approach constricted to analyses within a single taxa, typically yields dates of not more than about 5,000 to 10,000 years. Thus, when the hypothetical evolutionary constraints are removed, and the data is analyzed empirically, biblical timelines are achieved.

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# Ice age 'indicators' can form in warmer environments

Michael J. Oard

The idea that the bulk of the geological column formed during the Genesis Flood is challenged by claims that there were multiple ice ages in geological history, such as in the Permian. One supporting evidence used to justify such 'ice ages' is the presence of the pseudomorph<sup>1</sup> ikaite/ikaite/glendonite, which is claimed to only form in cold, glacial environments. A careful examination of the locations where these pseudomorphs are found reveals that they are not ice-age indicators and that all interpretations of past ice ages based on their occurrence are invalid.

Ikaite is a hexahydrate of calcium carbonate ( $\text{CaCO}_3 \cdot 6\text{H}_2\text{O}$ ) that forms spiky crystals of various sizes at near-freezing water temperatures. Calcite concretions sometimes form around its centre (figure 1). The macrocrystals found in sediments can be many centimetres long.

Ikaite was first discovered in the Akka Fjord of south-west Greenland. Since then, it has been noted in many high-latitude locations and in the



**Figure 1.** Ikaite with a calcite concretion at its center (wikipedia).

deep-sea environment of the Congo submarine fan. It is possible that it is present in other cold, deep-sea environments. Ikaite decomposes rapidly upon warming as it dehydrates. Sometimes the hexahydrate of calcium carbonate is replaced with calcite and retains the shape of the original crystal. It is then called a pseudomorph. Although these pseudomorphs have been given various names, glendonite is the most common.

## Glendonite assumed to be a proxy for near-freezing temperatures

Because the formation of ikaite is observed at near-freezing water temperatures, glendonite has been used as a proxy (or indicator) for near-freezing temperatures when it is found in sedimentary rocks:

"Although elevated levels of dissolved phosphorous may modestly increase the stability field of ikaite (Bischoff *et al.* 1993a) the relatively strict temperature limits on its stability make ikaite a robust indicator of cold water conditions and thus of great paleoclimate significance when its former presence can be detected in ancient sediments."<sup>2</sup>

As a result of this conclusion, glendonites are believed to form in a glaciomarine environment. This has been used to substantiate the uniformitarian Permian or late Paleozoic 'ice age'.<sup>3</sup> There are 30 geographic localities of glendonite in the Permian marine strata in the Sydney Basin, Australia, and this is used to support an 'ice age' interpretation of the sediments. This supposed 'ancient ice age' is assumed to have affected much of the southern hemisphere continents.

## Glendonite can also form in warmer conditions

However, glendonite is also found in sedimentary rocks formed under a

variety of conditions and of all 'ages'. This shows that it can form in warmer conditions as well. Glendonites have been discovered in mudstones and siltstones from the Precambrian to the present, including the Cretaceous and Tertiary, which are interpreted as being warm.<sup>3</sup> Except for the supposed 'ice age' periods throughout the geological column, and at the end of the Tertiary, nearly all of geological history is interpreted by uniformitarian scientists to have been warm, even at high latitudes.<sup>4</sup> This deduction is usually based on warmth 'indicators', such as fossils.

Because of this belief that glendonites are proxies for near-freezing water temperatures, some researchers have been forced to postulate a 'cold phase' during the warm periods. For instance, scientists have claimed a brief cold climate in the high latitudes during the Cretaceous 'greenhouse' period.<sup>5</sup> On Svalbard, the Norwegian archipelago in the Arctic Ocean at about 80°N, another cold phase during the very warm Paleocene and Eocene was claimed due to the discovery of rather abundant glendonites and 'erratics'<sup>6</sup> in Tertiary sedimentary rocks that were over 2 km thick.<sup>7</sup> Erratics up to 50 cm in diameter and weighing up to 150 kg are assumed to have been transported by ice. However, the sedimentary rocks also contained coal and have other warm climate indicators, although not in the same layer. This claimed 'cold phase' also goes against the current belief that the Arctic climate was surprisingly warm in the early Tertiary.<sup>8</sup> The Arctic Ocean has even been postulated to have been as warm as 18°C to 24°C at this time,<sup>9</sup> compared to an average Arctic Ocean sea surface temperature today of -2°C. These interpretations should have caused researchers to look for a mechanism for forming ikaite at warm temperatures.

The above discoveries are all found in the high latitudes and so uniformitarian scientists are able





**Figure 2.** Remnant of a landslide at the top of the Gravelly Mountains, southwest Montana, USA, that striated the bedrock. Outcrop is dated Eocene by uniformitarian scientists, and it used to be considered an ancient ice age because of two out of three 'diagnostic criteria'. Since the Eocene is now considered very warm, this ancient ice age had to be abandoned.

to claim a brief cold spell within a generally warm climate. However, some glendonites are found in mid-latitude strata, for instance in north-west Oregon and western Washington in the Miocene (early part of the late Tertiary).<sup>10</sup>

A recent discovery in northern Germany confirms that a warmer environment can also produce ikaite.<sup>11</sup> Abundant glendonites were found in what are considered to have been ocean-bottom sediments. Based on oxygen isotopes from fossils, the near-bottom temperatures were believed to be 10°C. Based on the carbon isotope values, the formation of the original ikaite is attributed to a nearby methane seep, with the methane allowing ikaite to form at warmer temperatures.

### Implications

Uniformitarian geologists used glendonites to reinforce the Permian 'ice age', but creationist geologists do not accept this claim because Permian

rocks are considered to have been laid down during Noah's Flood. Thus, we are wary of what are considered 'robust' proxies for past climate conditions. And with more research, when other variables and more data are considered, these proxies are found to be unreliable.

In this case, ikaite cannot only form in cold water but also in relatively warm water in the presence of methane. Confident uniformitarian paleoenvironmental interpretations are thus nullified by this further analysis and the consideration of neglected data.<sup>12</sup> Glendonites as a cold-climate proxy is shown to be no longer reliable. The rest of the indicators for the supposed Permian 'ice age', such as 'erratics', can be explained by massive downslope, underwater landslides during the Genesis Flood.<sup>13</sup>

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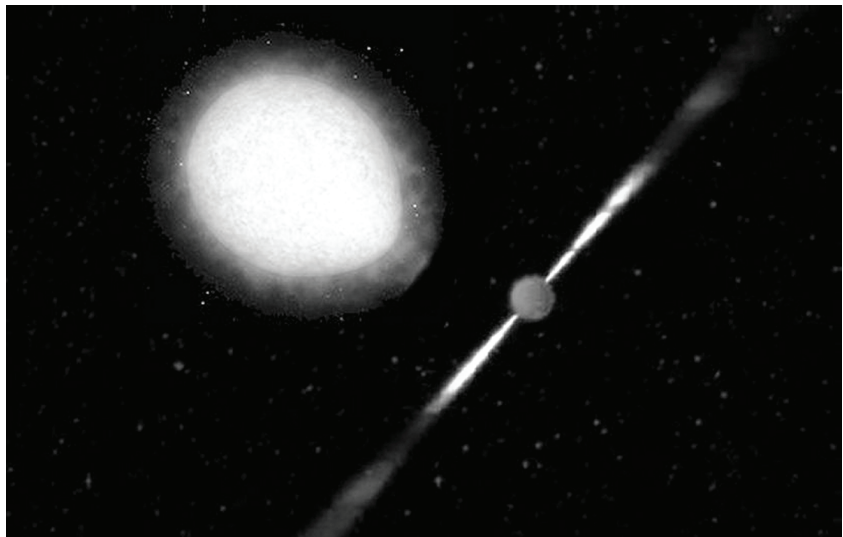
# The coolest White Dwarf—older than the age of the universe?

Ronald G. Samec

The discovery of an IMBP (Intermediate Mass Binary Pulsar, see figure 1) was reported in the *Astrophysical Journal*.<sup>1</sup> A pulsar is a neutron star that is the remnant of a compact core of a star emitting two flashes of light on each full rotation due to its strong bipolar magnetic fields. These flashes of light are emitted in north-south directions. This beam of photons is produced from accelerating electrons spiralling in intense magnetic fields. The surface magnetic field of the present pulsar is some  $7.2 \times 10^9$  Gauss as compared to the earth's 0.25–0.65 Gauss. The double flash (see figure 2) is due to the fact that the pulsar's two beams along magnetic axes are misaligned with the poles of rotation. The earth observer sees a stronger flash from the beam which is pointed nearer the earth than the other. So, two flashes result in each full rotation.

## Pulsars vs White Dwarfs

Pulsars are thought to arise from a supernova explosion which is due to an acoustic shock occurring deep within a massive star. The inner part of the star compresses until protons and electrons merge into neutrons creating a neutron star and the outer parts of the star blow outward and away from the star. The magnetic field of the star compresses into the compact core, making the intense magnetic field. This star had a companion, probably thought to be larger than the sun (but not massive enough to result in a supernova),



**Figure 1.** A White Dwarf and pulsar star binary. However, the White Dwarf in the present article is much darker.

which reached its last stages of life when it did not have sufficient fuel to continue its nuclear burning processes. In this case the theory says that the star steadily loses its outer gasses and ends its life as a ball of compact degenerate electron gas or a White Dwarf (WD). It may begin this stage with a very high temperature, say 50,000 K and it steadily cools over time following a well-known cooling rate. Eventually this object will cool so much that it will become a 'black dwarf' and will be disguised from observation as dark matter. However, this requires much more time than the age of the universe! This neutron star has a rather low mass of 1.2 solar masses and the WD 1.05 solar masses. The orbit is nearly edge on and the period of orbit is 2.4 days. The spin (rotation) period of the neutron star is rather long; 0.03 seconds.

## Problem 1—the orbit

One of the problems in this binary system is its low eccentricity. It has a near circular orbit. A supernova explosion happening nearby would certainly give an impulse to the orbiting star disrupting or ejecting it completely or at least adding energy to

its orbit, making it more eccentric. In fact, Type Ia supernovae are thought to completely annihilate after such an explosion.

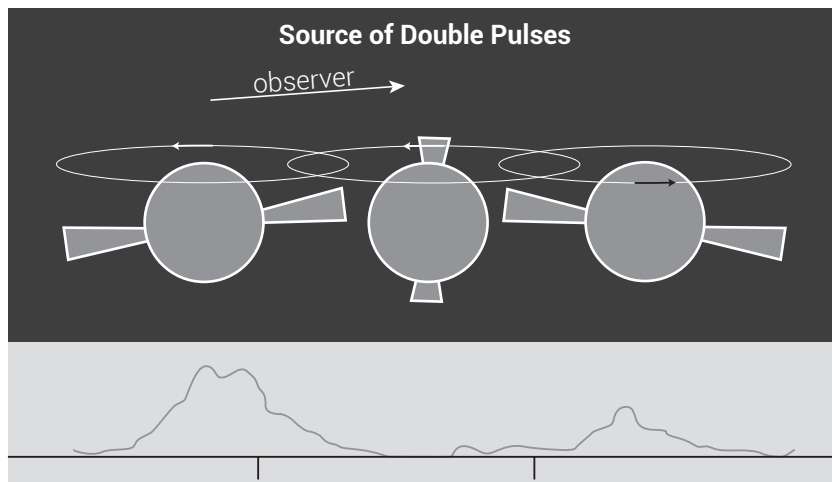
## Problem 2—the white dwarfs invisibility

But, the major trouble for evolutionary astrophysicists is that the White Dwarf is too faint to be observed with a magnitude  $>19.1$ . This makes it cooler than 3,000 K, the coolest WD on record! This is an upper limit. Other considerations give an upper limit as low as 1,700 K. It has to be a crystalized WD (or 'black dwarf' since it is optically invisible). For this to be the case it is probably older than the Milky Way (11 Ga). In fact the characteristic (spin down) age is 33.8 Ga old, much older than the universe (13.8 Ga) by a factor of 2.44 times! Much work is done by the journal authors to force its age into the limiting age of the Milky Way!

## The biggest problem—time

Another consideration is what was the time needed to become a White Dwarf? This must be added to the cooling age. The authors assume it





**Figure 2.** The pulsar has two beams along magnetic axes which are misaligned with the poles of rotation. The earth observer sees a stronger flash from the beam which is pointed nearer the earth than the other. So every rotation results in two flashes. The bottom plot is the observed light curve of the effect.

to have a rather high beginning mass of 6 solar masses. At this mass, the star could become a WD in 70 Ma. The authors must also be hoping that this object is among the first stars (population III), in which case, why are they applying the theory of normal stars in the galaxy to it (population I and II)? Another interesting idea that follows from this paper is that White Dwarfs become dark matter at below ~3,000 K! Thus, the neutron star is essentially being orbited by a dark matter star!

This situation highlights the problem of the cosmological ages in the universe. The 13.8 Ga scenario is obviously wrong even in creation time dilation based scenarios. Creationists have a real job sorting it out. One of the questions that need answering is: 'Are time dilation theories warranted?' This is still an open question. However, the idea that God created WDs is analogous to the idea that He created fossils in the ground, so they never actually lived and died. Thus they are a false history and any information they could lend to such creation topics as the Flood history and their historical appearance in the fossil record are moot.

### White Dwarfs tell us their past history

WDs likewise give us information about their past lives. For example, the type of WD gives us information about their earlier state (initial stellar mass). They are leftover remnants of low-to-intermediate mass stars. Low mass stars end up as Helium WDs. Solar type stars end as Carbon-Oxygen WDs. Stars on the higher end of the masses in question, as indicated in this paper, end as Oxygen-Neon-Magnesium WDs. (Of course, the authors can only interpret the type by the binary companion mass.) WDs are essentially 'fossil stars'. They have used up their fusion fuels and have lost their atmosphere and are left with degenerate electrons, slowly cooling over time. I believe that God did not create 'dead' stars.

On the other hand, if time dilation has operated, then the stars actually existed as normal stars and they have lived out their lives and ended as WDs. The information is scientifically accurate and no false history is conveyed by their appearance. Only the observer on the earth has observed them from a frame where time has slowed, so that these events *appear* to have all happened in a brief time

(inside a time period of less than 10,000 years). This all occurred in the past but how long ago did it happen in the *objects* time frame?

### Conclusion

The ages used by modern day astronomers are evidently wrong since they are based on evolutionary assumptions (the main one being the age of the sun which rests on radiometric dating of the 'oldest' meteorites). Creationist astronomers need to determine the apparent age of the cosmos by measuring ages of objects using alternate dating techniques that are readily confirmed (like orbital periods). That is the path I have taken.<sup>2</sup> My present research is pointed at the apparent evolution of binary star orbits. Their 'evolution' is found to be occurring much faster than what would be expected from theory.

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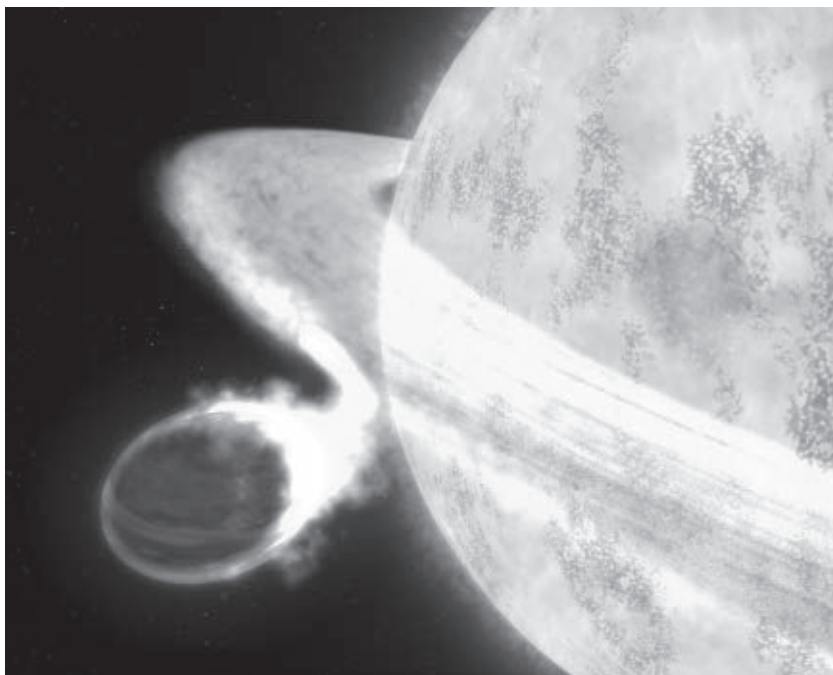
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# Exoplanets—habitable or not?

Wayne Spencer

Research on extrasolar planets gives much attention to finding Earth-like planets in what is referred to as the ‘habitable zone’ (HZ) of their stars. On one hand, modern techniques have had much success in finding exoplanets, yet a new challenge to habitability has presented itself. Often scientists search for dwarf stars to be candidates for habitable exoplanets. This is because a larger star would have its HZ farther from the star and the planets would be harder to find and detect, being farther from the star. Thus, exoplanets closer to their stars are easier to detect. There are now nearly 300 exoplanets that are considered in the HZ of their stars, as listed in the NASA Exoplanet Archive.<sup>1</sup> This generally implies the planet has a temperature range that is conducive to the presence of liquid water and possibly carbon dioxide in the planet’s atmosphere. Yet, it has been reported recently in a paper by Luger and Barnes that from models of the formation of these stars and their exoplanets, water could have been eliminated from these exoplanets early in their history.<sup>2</sup>

The Kepler space telescope provided many new exoplanet candidate objects through its precise transit measurements. As of 9 May 2015, NASA’s Exoplanet Archive<sup>1</sup> lists 8,662 exoplanet candidates from the Kepler space telescope detections. These possible exoplanets are known as Kepler Objects of Interest (KOI). Though the pointing mechanisms of Kepler partially failed in 2013, the Kepler spacecraft has been put back into service though in a somewhat less precise mode. Much extrasolar planet research has been turned towards confirming the detections and analyzing the results. Confirmed



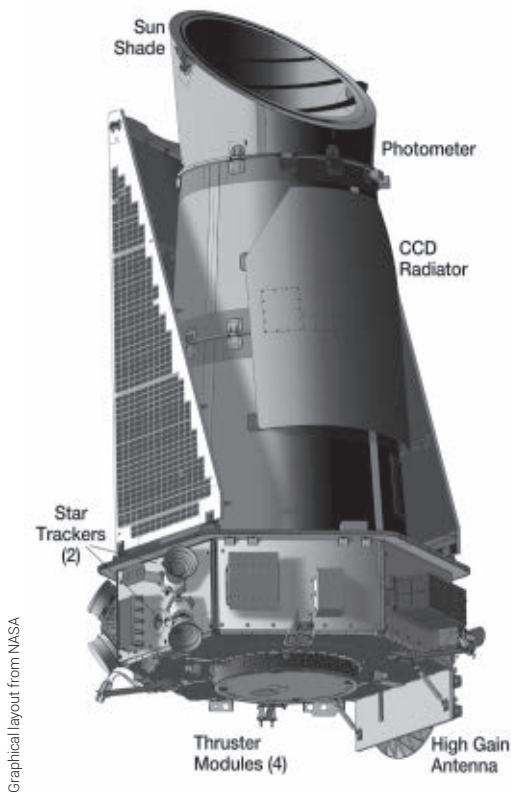
**Figure 1.** Artist's rendering of exoplanet WASP-12b. Gases and even metals are escaping the planet and falling into the star. Graphic from NASA and Wikipedia.

exoplanets from all detection methods are now 1,832 from the NASA Exoplanet Archive.<sup>1</sup> Of the KOI objects, the NASA archive lists 297 that are considered to be in the habitable zone. In the NASA Exoplanet Archive this is based solely on the radiation equilibrium temperature being between 180 Kelvin and 310 Kelvin. This is the temperature that an object would be at the given distance from the star based on the amount of energy it receives and reradiates.

## The habitable zone

The term ‘habitable zone’ has at least two definitions. The first is based on the equilibrium temperature of the planet primarily and has been called the ‘optimistic habitable zone’. In our solar system this would encompass the region from just inside the orbit of Venus to just outside the orbit of Mars. Another concept for the HZ has been termed the ‘conservative habitable zone’ or CHZ. The CHZ is defined based on climate models

and the greenhouse effect in a planet’s atmosphere. Thus the inner edge of the HZ would be where there is sufficient carbon dioxide, water, or other greenhouse gases in the atmosphere that there would be a runaway greenhouse effect. This would lead to the planet being too hot for life, similar to Venus. Then the outer boundary of the HZ would be at a distance where carbon dioxide in the planet’s atmosphere would freeze and fall onto the surface.<sup>3</sup> A recent source from 2013 put forward a modification of this ‘conservative habitable zone’ that specifically applies to cool dwarf stars such as class M dwarfs.<sup>4</sup> M dwarf stars are very common and are one of the most common types where exoplanets are detected. The number of M dwarf stars has generated a lot of optimism that there could be many possibly habitable Earth-like planets in our galaxy. It is indeed likely that there could be many exoplanets in our galaxy within the habitable zone based on the conservative definition above.



**Figure 2.** Cross-sectional design of the Kepler Space Telescope photometer instrument. Kepler is equipped with a 0.95 m (37 in) aperture Schmidt-type telescope and a 1.4 m (55 in) primary mirror. Kepler does not take photos but looks for dips in the light curve of a star that indicates a planet could be passing in front of it (called a transit).

But this in itself is no guarantee that life would be possible on such planets.

In 2014 Luger and Barnes brought attention to a new issue that makes habitability less likely assuming naturalistic formation models for stars and planets.<sup>2</sup> For dwarf stars, exoplanets tend to be very close to the star. According to stellar models, young stars are brighter and this can lead to processes that either drive water off the planet or cause photolysis of water vapour. M dwarf stars in particular tend to have very intense emission in the X-ray and extreme ultraviolet portions of the electromagnetic spectrum. The ultraviolet part can cause dissociation of water vapour. Secondly, if an exoplanet formed a significant atmosphere it is likely that the greenhouse effect would be intense

due to the intensity of the radiation from the star. The runaway greenhouse effect for planets very close to the star could be extremely intense and could also cause the dissociation of water vapour. Intense flare events could also have devastating effects for living things on exoplanets so near their stars.

The effect of the dissociation of water could be the build-up of oxygen in the exoplanet atmosphere (or external to the planet). The detection of oxygen around exoplanets could be mistaken by scientists as evidence of life, such as from the photosynthesis of plants. Thus, the combination of high temperatures near the star and destruction of water could make an exoplanet utterly barren of life, even though it is observed in the habitable zone. The authors make this statement about

the problem, “In general, we find that the initial phase of high luminosity may compromise the habitability of many terrestrial planets orbiting low-mass stars.”<sup>2</sup>

The migration of a planet from a distance inward towards the star would not change the basic problem because of the timeframes involved. Exoplanets near their stars would usually be assumed to have migrated inward because of the presence of a disk near the star as the system was forming, or from the influence of other planets that may no longer be present. During the inward migration the planet may not be hot enough to lose water. But as a planet migrates inward tidal forces tend to round its orbit. Then a debris disk could dissipate away or fall into the star and this would stop the

migration. Thus the planet could come to a stable orbit near the star where it may be very hot. The migration would typically be thought of as lasting several million years at most and there would still be long periods of time near the star that could ‘burn off’ the water.

## Conclusion

The study of extrasolar planetary systems is very relevant when one considers how these systems are different from our own. Our solar system is designed to be a safe and stable ‘neighbourhood’ for Earth, and Earth is designed for our benefit. In a young-age creation view, the exoplanets may have been created essentially as they are with little loss of water since creation. On the other hand, it is also possible that there could be significant loss of water and atmospheric gases from an exoplanet, even in several thousand years. Water vapour, oxygen, and other substances have been detected escaping from some exoplanet atmospheres into space. Naturalistic origins theories tend to come with their own liabilities. The changes in exoplanet atmospheres over time is an issue worth watching to see what develops from further research.

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# Only one glaciation observed in western Alberta, Canada—the ice-age reinforcement syndrome

Michael J. Oard

For about 60 years, from about 1910 to 1970, it was claimed that there were four global ice ages, give or take one.<sup>1</sup> This notion first arose with the recognition of four gravel layers in river valleys along the north slope of the Alps in Europe by Penck and Brückner in the late 1880s. These were correlated with the four ice ages believed to have occurred in America's Midwest. This correlation thus established the 'four ice ages' paradigm, which was reinforced with locations from all over the world that consistently claimed four ice ages.

It was once postulated that there were up to four glaciations in Alberta, based on deposits in river valleys and assuming the chronology in the US Midwest.<sup>2,3</sup> Since the ice is believed to have propagated from the same source area, the Laurentide Ice Sheet centred over Hudson Bay, ice is believed to have covered all of Alberta about four separate times just as previously thought for the Midwest.

However, all that changed with the acceptance of the astronomical theory of the ice ages in the 1970s. Uniformitarian scientists went from believing in four to accepting dozens of ice ages.<sup>1</sup> It is now assumed there were about 50 ice ages of various intensities based on deep-sea cores

during the past 2.6 million years of the Pleistocene within evolutionary/uniformitarian time.<sup>4</sup>

For instance, Stalker originally interpreted the data in Alberta as representing four ice ages.<sup>5</sup> However, once the astronomical theory of ice ages was accepted, and geologists concluded that there were many more than four ice ages, Stalker saw many more than four in his later papers. At a site near Pincher Creek, he summarized 26 tills of which most were of minor significance but 9 or 10 were supposedly major ice ages:

"The rest of the sequence consisting of till sheets with interfingering beds of alluvial and lacustrine sand, silt, and clay, is divided into fifteen units, nine or ten of which represent separate Laurentide ice advances."<sup>5</sup>

However, Jackson *et al.* pointed out:

"In this regard, Stalker commonly failed to clearly separate observation and interpretation. He routinely described glaciogenic diamictons as till with each serving as evidence for a separate glaciation. ... This led to his conclusion that there is widespread evidence of multiple glaciations throughout southern Alberta (rather than only in the eastern part of that region as we argue below). ... evidence for up to four glaciations were purported to be recorded by some sections such as the Brocket Section near Pincher Creek Alberta."<sup>6</sup>

In other words, both the 'four ice ages' and Milankovitch paradigms are classic cases of the reinforcement syndrome<sup>7</sup> that is ubiquitous within earth science.<sup>8</sup>

## One late Wisconsinan ice sheet over most of Alberta

However, it is becoming obvious that there was just one glaciation of the Laurentide Ice Sheet in western Alberta, occurring in what is

called the late Wisconsinan in the secular timescale.<sup>9–13</sup> Jackson *et al.* summarized the new information:

"Jackson and Little (2004) concluded that the last glacial maximum (LGM) was the only time that the Rocky Mountain Foothills of Alberta, Canada were glaciated by a *continental* ice sheet [emphasis original]."<sup>14</sup>

In fact, it was actually recognized back in 1961 that the glacial debris in Alberta generally showed one ice age and it was an assumption that there was more than one:

"Although it is generally recognized that Alberta has been glaciated more than once, no buried soils or other evidence of any long period between glacial deposits have been found."<sup>15</sup>

## Evidence for multiple glaciations can be explained by one ice age

But what about the apparently non-glacial sediments between till sheets that reinforced multiple glaciations? Jackson *et al.* showed that stacked till sequences in southern and central Alberta can be explained by one ice age:

"They [Jackson and Little, 2004] showed that stacked till sequences in this region can be related to belts of moraine and glacial limits dated to the *last* (Late Wisconsinan) glaciation ... It has also been documented in northern, central and south-central Alberta by radiocarbon dating or organic material in preglacial gravels underlying a single continental till in those areas."<sup>14</sup>

They go on to say that sand between till sheets can be deposited in one glaciation and that shearing at the boundary can cause multiple stacked till sheets with other deposits between.

Multiple layers of glacial till have been observed to form in Iceland. For instance, Evans and Twigg state: "Stationary glacial margins in

Iceland are capable of superimposing numerous till layers to produce large composite moraines ...”<sup>16</sup>. Multiple till layers can be also formed by thrusting till up and over other layers, or mass wasting of debris from within or on top of the glacier onto previously deposited till.

### Multiple ice ages mainly an assumption

The history of ice-age interpretation in western Alberta provides an instructive lesson: the idea of multiple glaciations has mostly been based on an earlier assumption:

“Glacial reconstructions commonly assume a multiple-glaciation hypothesis in all areas that contain a till cover. On the basis of demonstrated multiple events in the American Midwest, this assumption has been reasonable in Alberta Quaternary stratigraphic research [emphasis added].”<sup>17</sup>

Nevertheless, the authors tried to justify their assumption of multiple glaciations by pointing to the ‘demonstrated’ four ice ages in the American Midwest.<sup>18</sup> However, even the Midwest chronology has come under renewed scrutiny since the 1970s, probably because of the influence of the astronomical theory of the ice ages.<sup>19–21</sup>

Despite assumptions still used in interpreting the ice-age debris, especially the dozens of ice ages now assumed by the astronomical theory of the ice ages, the actual physical evidence shows there was only one ice age on the continents, consistent with the ice age model based on biblical history.<sup>22</sup>

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## Metamorphic rocks can form at shallow depths

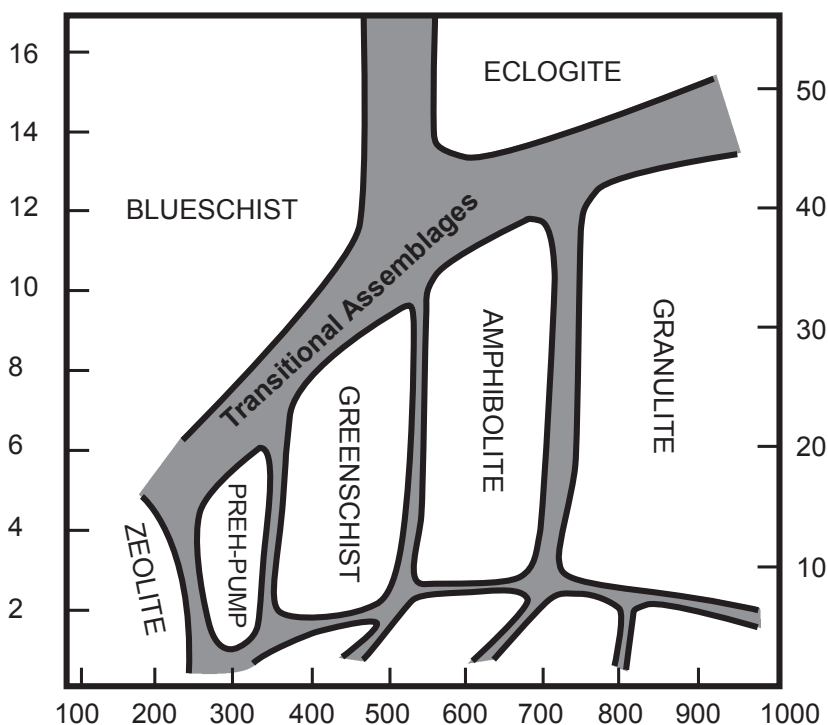
Michael J. Oard

There is much experimental evidence demonstrating metamorphic rocks can form at various pressures and temperatures (figure 1). Metamorphic rocks commonly crop out at contacts near and with igneous rocks (contact metamorphism and migmatites, respectively) and over broad regions (regional metamorphism). Using standard laboratory measurements, the metamorphic grade of the minerals provides an estimate of the depth of formation.

### The discovery of ultrahigh-pressure minerals

About 30 years ago, ultrahigh-pressure minerals (UHPm) were discovered.<sup>1</sup> They are usually inclusions in garnets, zircons, and other hard minerals believed to have formed at depths of over 100 km. UHPm include two rare high-pressure polymorphs of quartz, coesite (figure 2) and stishovite, and microdiamonds. They are found in isolated slices of presumed mantle rock and in more than 20 larger regions of the Earth called UHP terrains.<sup>2</sup> Scientists simply translate the metamorphic grade of UHPm to depth of burial.

It has been very challenging for scientists to explain why UHPm are found on the surface of the earth.<sup>3</sup> Most challenging is that nearly all of the UHPm are in what are believed to be continental rocks. This would require continental rocks to be forced downward to depths greater than 100 km, where it is believed high-pressure metamorphism takes place, and then ‘rapidly’ exhumed to the surface. Their idea of rapid, of course, means



**Figure 1.** Temperature-pressure diagram for various metamorphic facies. The pressure is considered the lithostatic pressure caused by burial depth.

at subduction velocities of 5 to 10 cm/yr within secular geological time.

Scientists have suggested that UHPm form in continental crust due to ‘continental collision’, or when a sliver of crust is dragged downward in a subduction zone and then somehow returns rapidly to the surface before the UHPm can undergo retrograde metamorphism back to low-pressure mineral phases. However, continental crust is less dense than oceanic crust and also less dense than the mantle below. How could less dense rock be forced down into more dense rock? This is where subduction has come to the ‘rescue’. At one time scientists firmly believed the continental crust was too light to subduct. Consequently, a paradigm shift resulted that now allows some continental crust to subduct. Many computer simulations have shown this process can occur *in theory*.<sup>4</sup> Despite the lack of empirical data, some scientists have now come to believe that their models

demonstrate a physical reality.<sup>5</sup> Others see these model results as premature conclusions:

“More-detailed and systematic field investigations are warranted to assess the predictions of numerical models, and more-sophisticated and realistic numerical models are required to replicate and explain the petrological, structural, and chronological data obtained from UHP terranes.”<sup>6</sup>

### Cracks in the paradigm change

Some scientists have suggested there are better possibilities than UHPm forming in subduction zones because they realized how difficult it would be for subduction zones to force continental rocks downward over broad areas of the Earth. Moulas *et al.* state: “However, there are well known cases where subduction has been excluded as a mechanism to explain

the exhumation of such rocks ...”<sup>7</sup> They continue:

“We conclude, based on these considerations, that geodynamic scenarios involving very deep subduction processes with subsequent very rapid exhumation from a great depth must be viewed with due caution when one seeks to explain the presence of microscopic ultrahigh-pressure mineralogical indicators in rocks.”<sup>8</sup>

However, there may be a somewhat easier solution. Experimental evidence shows coesite can form in high-stress environments at lower pressures.<sup>9</sup> Because metamorphism and deformation often occur together and the suggested depths of UHPm often seem too deep, Schmalholz, Podladchikov, and others suggested ‘tectonic overpressure’.<sup>10,11</sup> Tectonic overpressure is added stress caused by tectonic movement or convergent forces within the rock. That would allow UHPm formation at depths less than half of those expected—less than 50 km deep as a possibility.<sup>12</sup>

Many scientists reject the idea of tectonic overpressure because they think the amount of tectonic pressure is too large to be realistic.<sup>13</sup> They also concluded stress in the earth is generally the same in all directions (isotropic).<sup>14</sup> Consequently, they do not include tectonic overpressure to their models. Isotropy can also be a poor assumption, since differential stress is rather common in Earth’s crust and upper mantle due to tectonic forces and/or differences between fluid and rock pressures in porous rocks.<sup>15</sup>

### Scientific implications

A number of implications follow from the discovery that coesite can form at lower pressures in high-stress environments. First, if tectonic overpressure is a possibility, deductions that were based on the metamorphic grade and depth of burial may need to be re-evaluated:



“If this is true, then Wheeler’s result has considerable consequences for geological applications, because it is commonly assumed that the metamorphic reactions are controlled by the lithostatic pressure (the weight of the overlying rock) which can be directly related to depth. ... If minerals might not be reliable indicators of maximum burial, then one might fear that metamorphic petrology could lose one of its main applications. However, if tectonic pressure and differential stress could indeed considerably influence metamorphic reactions, then this could also create new applications.”<sup>11</sup>

Second, the discovery of low-pressure coesite demonstrates that we still do not understand many aspects of geology and geophysics, and what we thought we knew, may not be correct.

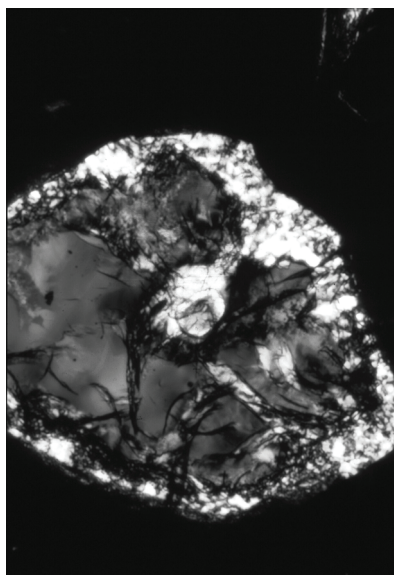
Third, this example shows that when a new variable is added to a concept, it can change the results as well as the applications.<sup>16</sup> We should therefore be aware that uniformitarian interpretations of the past based on

rocks, fossils, and geophysics are tentative.

Fourth, we need to be skeptical of models claiming to demonstrate a past event. Models are marginally useful for many reasons and are only as good as their input parameters and assumptions.<sup>17</sup> Often there is a lack of knowledge about the variables and their interactions, which are often non-linear. Furthermore, even if all of the information about all of the variables were known, the lack of complexity of the software would still be a major limiting factor. Because of these difficulties, many variables are estimated. This increases the likelihood of error. The many models used to explain UHPm mask the underlying uncertainties.

### Creationist implications

Tectonic overpressure is couched in a uniformitarian context of non-catastrophic tectonic forces. The catastrophic Flood models have the potential to develop much greater tectonic overpressure because they are not limited to slow uniformitarian rates that are observed today. In the CPT model, plate movements of metres per second have the capability to create greater tectonic pressure at shallow depths and provide a better explanation of zones of UHPm. Meteorite impacts, powerful volcanism, catastrophic plate tectonics, and rapid differential vertical tectonics would add more stress to the earth than uniformitarian science assumes. As a result we are in a better position to explain how UHPm formed, possibly at depths shallower than 50 km. Meteorite impacts are well known to produce coesite, shistovite, and microdiamonds.<sup>18</sup> Further investigation will improve our understanding of UHPm and our Flood models. It is important to remember that Flood models are still in their infancy and are also limited by software capability and unknown variables.



**Figure 2.** Coesite grain, 1 mm across, with a small inclusion of pyroxene in the center, surrounded by eclogite.

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# Can 'megasequences' help define biblical geologic history?

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For over two centuries, naturalistic geoscientists have laboured to construct an Earth history from sediments, rocks, and fossils found in nature. Initiated in France in the late 1700s, then subsumed and more fully developed in succeeding years in Great Britain, stratigraphic correlation and geologic mapping spread across continental Europe and subsequently to North America. Problems developed early in the 20<sup>th</sup> century with correlation discrepancies between North American chrono- and biostratigraphic facies and formal 'British' geologic periods. By mid-century, an apparent resolution came through the application of transcontinental, time-equivalent stratigraphic unconformities, which defined six bounded 'Sloss stratigraphic sequences'. These sequences have been adopted and labelled 'megasequences' by several young-earth creationists. We question the adaptation and utility of Sloss sequences in defining biblical geologic history since the naturalistic-uniformitarian geologic timescale is used to define them and their corresponding unconformity boundaries.

**S**tratigraphy is the study of rock layers, and more formally: "The science of rock strata. It is concerned not only with the original succession and age relations of rock strata but also with their form, distribution, lithologic composition, fossil content, geophysical and geochemical properties indeed, with all characters [sic] and attributes of rocks as strata; and their interpretation in terms of environment or mode of origin, and geologic history. All classes of rocks, consolidated or unconsolidated, fall within the general scope of stratigraphy."<sup>1</sup>

Throughout the early to mid-1800s, French, then British, naturalistic stratigraphers matched sediments and fossils to develop local-to-regional geologic maps and corresponding geologic columns<sup>2</sup> (figure 1). Stratigraphic correlation proved successful across many areas (e.g. Paris Basin, Great Britain), and was applied across North America.<sup>3,4</sup>

An article published in 1949 by several North American geologists noted discrepancies between the British time-stratigraphic and biostratigraphic divisions (as defined by the naturalistic geologic timescale) and North American strata due to differences in facies (i.e. sediments and fossils) as a result of variations in tectonic influences.<sup>5</sup> They proposed a new approach based on the division of strata by transcratonic unconformity boundaries. They divided the strata spanning the North American craton into six 'Sloss stratigraphic sequences'.<sup>6,7</sup> Sloss's ideas regarding unconformity boundaries were later developed through seismic stratigraphy into sequence stratigraphy.

In recent years, several young-earth creationists have begun to advocate use of these Sloss sequences, which they have labelled 'megasequences'. This growing popularity revives the unresolved debate over the role of the naturalistic

geologic timescale in Flood geology.<sup>8</sup> Sloss's idea of focusing on unconformities is innovative and intriguing. Can transcontinental stratigraphic sequences be discerned by broad, bounding unconformities, and can they be used in the development of biblical geologic history? We will review the Sloss proposal for multiple stratigraphic sequences, the derivative creationist 'megasequences', and their relevance and application to Flood geology.

## The development of stratigraphy

The study of stratigraphy predates today's naturalistic-uniformitarian philosophies of Earth history. In 1671, Nicolaus Steno established the first rules of stratigraphy,<sup>9</sup> which were followed more than a century later with the publication of the first geologic maps of the Paris Basin (1808) and much of Great Britain (1815).<sup>10–12</sup> Through the auspices of the Geological Society of London, these maps were used by deists and agnostics to develop and refine the 'Wernerian' Plutonist philosophy of Earth history as a naturalist alternative to the biblical history of the Earth.<sup>13,14</sup> Under this new philosophy, stratigraphic correlation became the tool to subdivide and refine stratigraphy into a broader, more organized geologic column and corresponding timescale.<sup>15–18</sup>

## Time-stratigraphic and biostratigraphic divisions

These ideas also advanced the geologic mapping in North America, and further developed from simply matching sediments and fossils to defining specific 'facies' and 'facies analysis'—reconstructing past environments. According to Sloss *et al.*:





the structural aspects of each layer. To the writers, the horizons or surfaces separating these complex units of strata represent repeated episodes in the history of the mid-American craton during which the tectonic behavior of the craton abruptly changed, causing significant changes in the character of deposition. *These abrupt changes are reflected by marked discontinuities in the stratal record of the craton which may be traced and correlated for great distances on the objective bases of lithologic and faunal ‘breaks’, and continuity in distribution and facies, of the transgressive strata found above the discontinuities* [emphasis added].”<sup>24</sup>

More simply stated, the naturalistic assumption of any transcontinental unconformity boundary would require the assumption of continent-spanning erosional events correlated through application to their geologic timescale (see Appendix I).

### Emphasis on unconformities

The idea of dividing strata into stratigraphic sequences developed because the formal stratigraphic divisions of the British-derived geologic timescale did not directly correspond to North American regional unconformities.<sup>5,7,25,26</sup> To alleviate this problem, Sloss and his co-authors decided to name each stratigraphic sequence after a Native American tribe.<sup>27</sup> This resulted in six sequences, which he named (oldest to youngest): 1) Sauk Sequence, 2) Tiptecanoe Sequence, 3) Kaskaskia Sequence, 4) Absaroka Sequence, 5) Zuni Sequence, and 6) Tejas Sequence.<sup>5,7</sup> The genius in this approach was a change in focus to unconformities, and that the laborious identification of fossils and the correlation of sediments was of less emphasis. Strata could be grouped together and tied to the timescale solely from matching bounding transcontinental unconformities. Sloss<sup>28</sup> was careful to craft this new concept in a manner that did not challenge the British-derived geologic timescale:

“Although sequences have a greater time stratigraphic significance than classical rock units ... there is no implication in the sequence concept of an attempt to establish a North American, as opposed to a Western European, time scale.”

An important point recognized by Sloss *et al.*,<sup>29</sup> but commonly overlooked in the subsequent work of others, was that the unconformity boundaries are not chronostratigraphic:

“... the horizons or surfaces separating these complex units of strata represent repeated episodes in the history of the mid-American craton during which the tectonic behavior of the craton abruptly changed, causing significant changes in the character of deposition. These abrupt changes are reflected by

marked discontinuities in the stratal record of the craton which may be traced and correlated for great distances on the objective bases of lithologic and faunal ‘breaks’, and continuity in distribution and facies, of the transgressive strata found above the discontinuities. *These discontinuities were not formed simultaneously over the entire area of their extent, since the tectonic and environmental conditions they represent were initiated earlier in some areas than in others. Therefore, these surfaces or horizons must not be considered as time planes universally referable to the same positions on the geologic calendar. Instead, they should be treated as objectively operational datum horizons which may be readily recognized in outcrop or well records and used to differentiate the stratigraphic column* [emphasis added].”

Surprisingly, Sloss *et al.*<sup>30</sup> also claimed the variability of the strata within the individual sequences was not defined by specific time intervals:

“Sequences should be considered as rock units, assemblages of formations and groups. They are simply the strata which are included between objective, recognizable horizons, and are without specific time significance since their limits do not coincide with time lines and may include rocks of different ages in various areas.”

However, this claim ignores the fundamental and pre-existing links between the strata and the timescale. Strata had already been classified by age, and all implicit correlations were made on that basis, as evidenced by the stability of the conceptual timescale in its basic structure from before the exploration of most of Earth’s geology. This is evident in later references to the sequences that use the timescale’s ages to define them (figure 2).

### Stratigraphic sequences

The six Sloss sequences are defined by their bounding interregional (i.e. transcontinental) unconformities. The initiation of each sequence began with a transgression (sea-level rise) and it ended with a regression (sea-level fall sufficient to expose the craton to erosion). Sloss stated:

“Each sequence represents a major transgression and overlap, beginning at the cratonic margins and in the basins of greatest subsiding tendencies, gradually spreading to the more stable areas of the cratonic interior, and ultimately lapping up on the margins of the Canadian Shield. The transgressive phase, buried and protected by a cover of younger strata, is commonly well preserved. The closing regressive phase of each sequence is typically poorly preserved, since the representative sediments were exposed to

erosion at the close of the major depositional cycle of which each sequence is a record. In most cases sufficient testimony is preserved to indicate clearly that each sequence is representative of a major cycle of transgression, commonly complicated by minor reversals in trend and by a host of local effects.”<sup>31</sup>

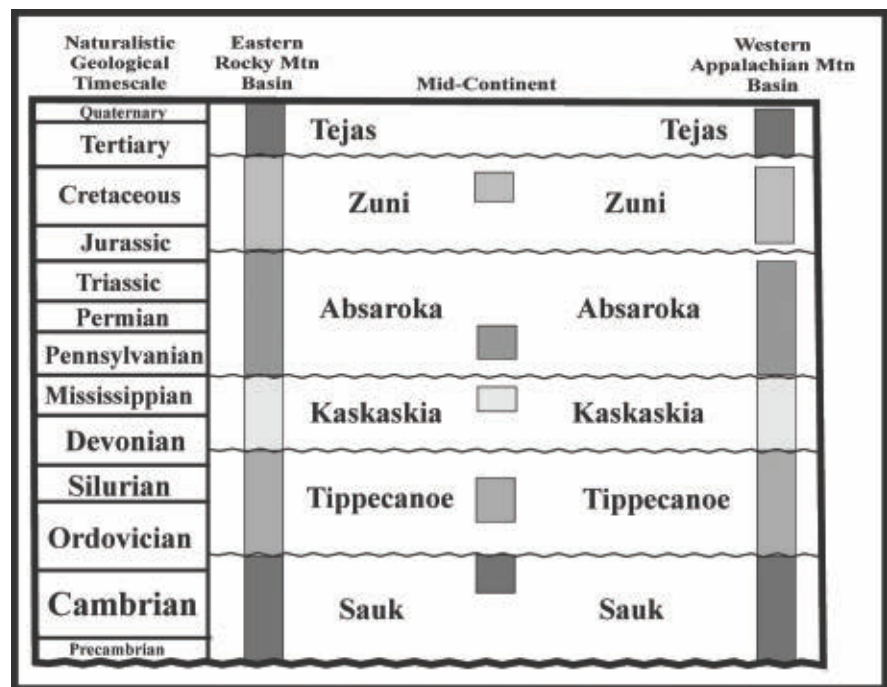
Sloss clearly recognized the limitations of these sequences:

“The cratonic sequences are rock units defined by unconformities and of broad although finite, lateral extent. Therefore, the utility of the six sequences of the present paper in interpreting the geologic history of the North American craton notwithstanding, ... they have no necessary applications to the rock stratigraphy and time stratigraphy of extracratonic or extracontinental areas.”<sup>32</sup>

However, as modern seismic stratigraphy developed in the early to mid-1970s, Sloss believed his sequence-bounding surfaces could be extrapolated across all cratons “and may be considered global cratonic unconformities.”<sup>33</sup> Each of the six Sloss<sup>5,7</sup> sequences presents a high level of stratigraphic variability. More importantly, each sequence is bounded at its base and top by perceived transcontinental unconformities. In reality, these unconformities cannot be physically traced across the continent but are projected by connecting ‘correlative conformities’.<sup>34,35</sup> These correlative conformities are aligned on the basis of their age, as dated by the geologic timescale.

### Modern sequence stratigraphy

Beginning in the 1970s with the advent of seismic stratigraphy, former students of Sloss modified the application of unconformity boundaries from transcontinental to regional scale. This smaller-scale approach was directed toward the pursuit of petroleum hydrocarbons across sedimentary basins and became the framework for modern sequence stratigraphy.<sup>36</sup> While conceptual similarities exist between Sloss sequences and sequence stratigraphy, differences exist in scale, roles of tectonism, variations in sea-level change,



**Figure 2.** Three stratigraphic columns with the six Sloss sequences extending from the Rocky Mountain Basin to the central continent, to the Appalachian Mountain Basin. Note the thickening and thinning of the sequences (shaded boxes) as a consequence of developing basins, erosion, or non-deposition. This variation in strata and corresponding age is what Sloss *et al.*<sup>5</sup> claim as sequences without time. However, this is misleading because the change between the individual stratigraphic columns is due to the size of the missing strata and corresponding unconformity. The loss of strata in some areas demonstrates that sequences may have more gap than record (i.e. more rocks are missing than present—which is a function of the geologic timescale and not what the actual rocks exhibit—see Ager<sup>86</sup>). Diluvialists must consider the possibility that much of the ‘missing time’ is illusory. (After Sloss.<sup>87</sup>)

and objectives.<sup>37,38</sup> Possible application of modern sequence stratigraphy to Flood geology has been discussed by several young-earth creationist geoscientists (Appendix II) and is outside the focus of this paper.

### Sloss stratigraphic sequences transformed into creationist ‘megasequences’

The use of Sloss sequences has been advocated by several young-earth creationists. Austin and Wise<sup>39</sup> invoked the initiation of the Flood in the Grand Canyon with the deposition of the Sixtymile Formation, and correlated it to the Kingston Peak Formation across the Mojave region, westward across southern California. Both formations are viewed as the base of the Sauk Sequence, which they renamed a ‘megasequence’.<sup>40</sup> These stratigraphic units onlap the top of the Great Unconformity.

Austin and Wise<sup>41</sup> also identified the erosional base of the overlying Tippecanoe Sequence but did not convey the reasoning for its position in the study area. No other Sloss<sup>7</sup> sequences were identified. To correlate the stratigraphic units across Arizona, Nevada, and California, Austin and

Wise<sup>41</sup> used regional stratigraphic correlation charts to match the formations. However, they defined the base of the Sauk Sequence using five discontinuity criteria.

American geologist Gordon Davison<sup>42</sup> also invoked megasequences but expanded their number and location across the globe. He advocated abandoning the geologic timescale and sought to tie them to “coherent subdivisions of geologic time within a single tectonic domain during the Flood”.<sup>43</sup> This approach would discount the stratigraphic correlation of sediment and fossils and emphasize the importance of the depositional tectonic framework corresponding to the flux of geologic energy during the Flood. Unfortunately, this promising work has not been further developed.

In 2009, Australian geologist Andrew Snelling reviewed the Sauk Sequence in the Grand Canyon<sup>44</sup> based on the work of Austin and Wise,<sup>39</sup> and agreed with their conclusion that the Cambrian Tonto Group, specifically the base of the Tapeats Sandstone, is the base of the Sauk Sequence. However, Snelling extended the ‘Sauk Megasequence’ well beyond the area discussed by Austin and Wise:

“The vertical sequence consisting of the Great Unconformity, Tapeats Sandstone, Bright Angel Shale, and Muav Limestone has enormous horizontal extent, which can be measured in terms of many hundreds of kilometers. However, the Sauk Megasequence, which consists of these Tonto Group strata in the Grand Canyon region, has been traced right across the North American continent, because strata units similar to those which make up the Tonto Group can be correlated with one another over such an enormous lateral extent. Indeed, it is possible to map the occurrence of all the sandstone strata that correlate with the Tapeats Sandstone, which together are known as the basal sandstone lithosome of the Sauk Megasequence. Distribution of this basal sandstone lithosome appears to form a single sandstone body that blankets a major portion of North America, extending along the Mexico border from southern California to Texas northwards across Montana and much of North Dakota through to Canada, and from southern California and Nevada right across to the Mid-West and the [sic] New England including Maine.<sup>45</sup> As such, this enormous blanket of sandstone right across North America represents a major flooding of the land, the evidence in the Tapeats Sandstone implying that it was a rapid, storm-driven inundation, such as that which occurred at the initiation of the cataclysmic Flood event.”<sup>46</sup>

More recently, Snelling<sup>47</sup> reviewed the six Sloss stratigraphic sequences but only attributed five of them to the Flood. In defining these sequences, he stated:

“Geologists have discovered that powerful forces eroded the entire North American continent, and then deposited the debris over the whole continent. This was repeated several times. How is this possible? The obvious answer is the Flood.”<sup>48</sup>

He omitted the uppermost Tejas Sequence (which is also considered by naturalists to be transcontinental and comparable to the other five Sloss sequences) and did not convey his reasoning in its omission, although he possibly believes it to be post-Flood deposits.<sup>49</sup> Still unresolved is the problem of likely chronological stratigraphic discontinuities in a single conceptual continental-scale transgression and regression ‘Flood sequence’. Also, Reed<sup>50</sup> noted that similar stratal packages may represent similar *processes* operating at *different times* during the Flood, since topographic and lateral distances would cause time differences that would be significant in Flood deposition.

Young-earth creationist Clarey reported on the results of his analyses of transcontinental Sloss stratigraphic sequences, which he also defines as ‘megasequences’:

“Using data from over 500 stratigraphic columns, I examined megasequences across North America to document the sedimentary evidence for the Flood’s catastrophe. At each site, the megasequence boundaries were identified, along with the thicknesses and extent of individual rock types.”<sup>51</sup>

A new seventh megasequence was identified by Clarey at the Midcontinent Rift of North America:

“Preliminary results demonstrate the presence of a seventh megasequence below the six common fossil-bearing megasequences. It lies just below the Sauk Megasequence in what secularists [i.e. naturalists] call the late Precambrian or Proterozoic Era. However, this newly delineated pre-Sauk sequence may be instrumental in documenting the onset of the Flood.

“In part, the pre-Sauk megasequence was created by a tremendous outpouring of basaltic lava that split open central North America and caused the Midcontinent Rift. ...Could this be evidence of the breaking up of the ‘fountains of the great deep’ mentioned in Genesis 7:11?”<sup>51</sup>

It should be noted that Reed previously published an extensive review of the Midcontinent Rift from a young-earth creationist perspective and proposed rift initiation at the onset of the Genesis Flood. However, because it occurred in the *interior* of North America, far from any transgressing ocean, there would have been a period of tectonism/volcanism and rainfall-induced sedimentation (from local flash floods infilling basins) prior to the initial Flood marine transgression, when broader-scale marine transgression as floodwater moved into this area:

“The MRS [Midcontinent Rift System] can be



explained as an event marking the initiation and early stages of the Genesis Flood in the northern Midcontinent region. Field evidence strongly suggests that structural downwarping, crustal fracturing, erosion, sedimentation, and volcanism began almost concurrently. The language of Genesis 7:11 implies that the initiation of geologic activity associated with the Flood was sudden and intense. The Flood model requires local erosion, limited transport, and rapid deposition of sediment in an environment created by heavy continuous rainfall. A vertical and lateral change to regional erosion, longer transport distance, and regional deposition marks the transition to conditions associated with the advancing transgressive front.

*“The ... loss of ... the geologic column in the northern Midcontinent would undermine uniformitarian models, the current understanding of natural history, and radiometric methods implying the long hiatus [emphasis added].”<sup>52</sup>*

Note that Reed<sup>52</sup> sees a discrepancy between the necessary continuous timing of events at the Midcontinent Rift System in the diluvial framework and the naturalistic proposal of an approximately 500-million-year hiatus between rifting and subsequent Cambrian marine transgression; since the time of this hiatus is equal to the time of the entire overlying rock record, and since the craton should have undergone cycles of transgression and regression on a more frequent basis.<sup>53</sup> Clarey’s detailed work remains unpublished, and we look forward to seeing how he handles these problems.

## Discussion and conclusions

The use of regional-to-continental scale unconformities to define stratigraphic sequences is an area that may be fruitful for creationists. However, the existing unresolved problem of how the naturalistic geological timescale applies to diluvial geology will probably affect future work, since Sloss sequences have an inherent bias towards the timescale, as well as toward the uniformitarian/evolutionary view of history. For those advocating the incorporation of a compressed chronostratigraphic timescale, the Sloss<sup>7</sup> concept will be used in the same way—simply by ignoring the geochronologic ages, but using the chronostratigraphic timescale in its ‘Hadean to Holocene’ framework.

We advocate returning to the field data and rebuilding a stratigraphic understanding from that data, within the framework of biblical history. The point of disagreement is *not* whether to accept geologic observations; it is how to recognize and address naturalistic presuppositions that are embedded in modern stratigraphy—down to its foundations. For example, naturalistic geologists see *time* as the conceptual

foundation for global stratigraphic correlation. This follows from their uniformitarian, deep-time perspective, which views the rock record as a series of snapshots (of similar processes) that can be assembled into a coherent story of Earth’s evolution. However, if the bulk of geologic activity occurred in a single year, is that perspective valid? If not, how does it affect our understanding of the timescale?<sup>54</sup>

The heart of the issue of using Sloss-based megasequences is their dependence on the geological timescale. One creationist school of thought is rejecting absolute dates—the geochronological timescale—from the chronostratigraphic timescale, the relative arrangement of strata by their chronology (i.e. Hadean to Holocene). This seems attractive because it follows the division noted by secular geologists. These creationists think that rocks can be identified and correlated by reference to the chronostratigraphic scale, and then connected to biblical history. However, we disagree. If we are right, it undermines the use of megasequences because they are correlated also by reference to the chronostratigraphic timescale.

A related problem comes from the nature of unconformities. They are seen by naturalistic geologists as evidence for long periods of erosion or non-deposition. Diluvialists cannot accept this conclusion. What if we view these unconformities—even regional ones—as evidence of rapid hydrodynamic action?<sup>55</sup> We know that, on observable scales today, factors as simple as changes in current velocity, depth, or sediment supply can create local unconformities. Might not some larger-scale unconformities reflect similar, but Flood-scale, processes? If so, how might that affect our understanding of ‘megasequences’? These factors all need careful consideration.<sup>56</sup>

The presence of these (largely unaddressed) assumptions is the reason we urge caution in the application of ‘megasequences’ in Flood geology. All such sequences are ultimately constructed from the naturalistic geological timescale. Physical correlation, independent of the timescale, spanning entire continents remains to be demonstrated, although the presence of widespread, lithologically similar strata certainly suggests possibilities of large-scale interpretation.<sup>55,57</sup> Stratigraphic, tectonic, and hydrodynamic considerations must all play a role in defining the actual rock record.<sup>58</sup> Naturalistic methods and assumptions will be of less utility. For that reason, the use of naturalistic, regional-scale stratigraphic correlation charts in defining creationist megasequences should proceed with extreme caution. The idea that strata across the North American continent were deposited ‘simultaneously’<sup>59</sup> in layer-cake form is violated empirically<sup>60,61</sup> as well as conceptually.<sup>38,62,63</sup> The North American continent contains areas of uplift adjacent to developing basins. Each area/region will need to be examined from basement to surface to reconstruct its

biblical geologic history. Questions to be answered include criteria for assigning parts of the crust and overlying rocks, sediments, and fossils to the Creation Week, the Flood, Ice Age, and subsequent millennia (figure 3). Then, we must interpret those parts of the rock record according to events commensurate with each episode, not with the outworn

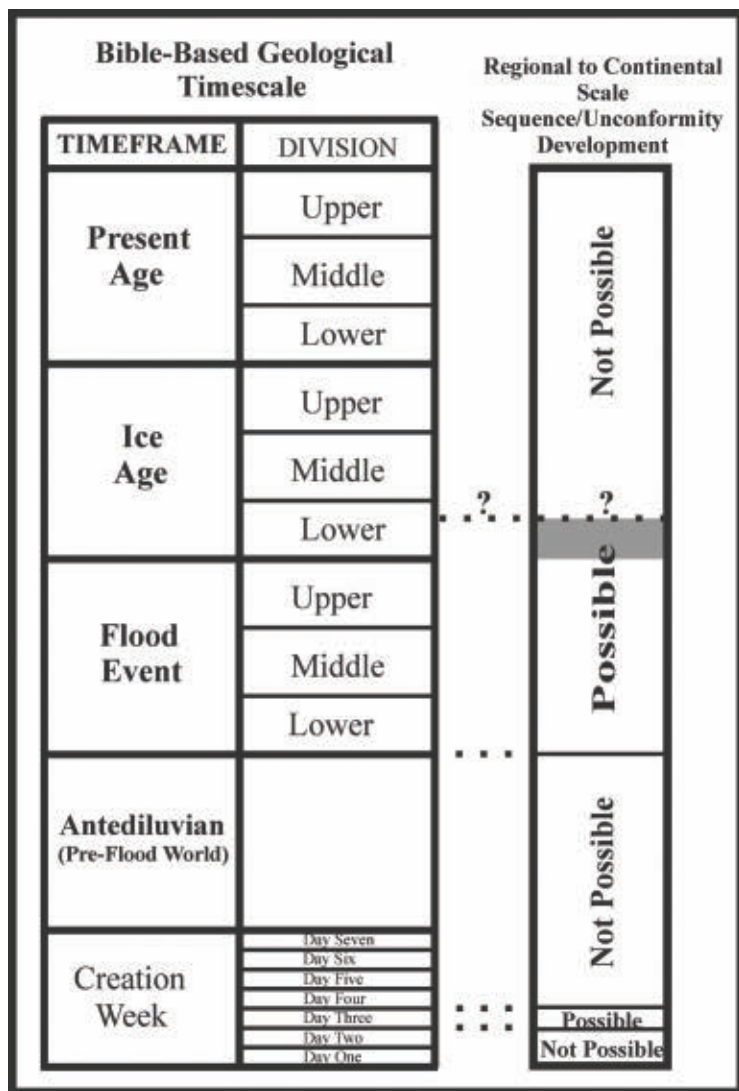
actualism of naturalistic geology. Time may have much less to do with stratigraphic sequences than do tectonic or hydrodynamic energy.<sup>64</sup>

Unconformity boundaries and strata should be correlated as broadly as possible, but we should be sure that the empirical correlation criteria are observed, and that correlation is not

extrapolated based on uniformitarian time. We must also remember that similar Flood processes, occurring at different times, could result in very similar strata. The approach of Austin and Wise<sup>39</sup> for defining the pre-Flood erosional surface at the top of the Great Unconformity is consistent with biblical Flood-related expectations, but a case can also be made in other areas for the Flood onset at the top of the basement contact.<sup>65</sup>

The six Sloss sequences<sup>7</sup> may have application to biblical history, but their usefulness can only be determined independently, and not simply transferred into Flood geology without examination of all naturalistic assumptions. Conceptually, the onset of the Sauk Sequence with the transgression of the ocean across a continent is consistent with the expectations of the Flood. But it also raises questions regarding the pre-Flood Earth surface—was it all basement rocks? Additionally, the repeated cycles of transcontinental transgression and regression creating regional unconformities between Sloss sequences appears to be inconsistent with the biblical record, which records one global transgression–regression cycle, not six (Genesis 7:17–20). Work remains to be conducted and it will likely require independent thought and unique solutions inconsistent with the philosophy of Naturalism.

We contend that biblical geologic history cannot be defined on an internally consistent basis using the naturalistic geologic timescale. For that reason alone, there is a heavy burden of proof on those who wish to simply apply Sloss sequences to Flood geology. The basic methodology may work well, but *only* when *all* uniformitarian baggage is eliminated. It is unlikely that Sloss sequences can be imported into Flood geology without careful analysis of stratigraphic implications. As currently defined, proponents of young-earth–creationist use of Sloss sequences have not yet met that standard. We hope that researchers will address all of these issues and define better ways for interpreting the rock record in the context of the history conveyed in the Bible<sup>64–67</sup> (figure 3).



**Figure 3.** A Biblical Geologic Timescale with potential time intervals where transcontinental sequences and their bounding unconformity boundaries could develop. The grey shaded area may represent a time when local/regional unconformities were created, based on three possibilities: 1) floodwater withdrawal was occurring at different rates across the continents;<sup>88</sup> 2) large-scale vertical tectonic movement may have displaced/advanced floodwater across areas at the close of the Flood Event timeframe, and 3) glacial waxing/waning during the singular Ice Age timeframe may correspond to sediment deposition/erosion due to glacial eustasy. Further study in all three cases is warranted. We do not define/correlate any sequences within this framework because that work has not been conducted. A serious problem remains in explaining the multiple transcontinental transgression–regression cycles of floodwater movement required to match the six Sloss sequences. It should be apparent that the naturalistic geologic timescale (figure 1) and this biblically aligned timescale do not allow direct correlation.<sup>56</sup>

## Appendix I

Sloss's concept of continental-scale 'layer-cake stratigraphy'<sup>24</sup> has gained broad acceptance in North American stratigraphy.<sup>5,7,22,23,68</sup> This idea holds that strata (with matching sediments and fossils) were deposited across vast regions and can be correlated by reference to a specific period of time (see figure 1). However, this is *only* possible through application of the uniformitarian geologic timescale. While geologists divide that timescale into chronostratigraphic and geochronologic parts, the rejection of biblical history is built into both.<sup>69–71</sup> The attempt to divorce 'time' from the timescale and use the 'stratigraphic data' (though they are themselves correlated by the chronostratigraphic timescale) as an empirical global geologic column ignores inherent anti-biblical assumptions and methods.<sup>72,73</sup>

Naturalistic geologists have constructed innumerable stratigraphic correlation charts (e.g. American Association of Petroleum Geologists, Correlation of Stratigraphic Units of North America) that identify vertical stratigraphic profiles for a particular area or region. These charts are especially useful in correlating strata across distant locations. But the framework remains the conceptual template of the naturalistic timescale. We fail to see the benefit to diluvial geology in following a compressed chronostratigraphic timescale,<sup>74</sup> which was built on the philosophical foundations of men determined to suppress biblical history. As such, in as far as megasequences are identified on the basis of correlation with the chronostratigraphic timescale, their utility in the biblical framework is questionable. Those who wish to adapt megasequence analysis to the biblical framework must demonstrate that the basis for correlation to identify megasequences is independent of the chronostratigraphic timescale, or that another basis for correlation exists.

## Appendix II

Modern sequence stratigraphy has been discussed at length by several young-earth creationists and will not be repeated here. It is important to note that two opposing philosophies exist,<sup>56</sup> with one following a compressed chronostratigraphic timescale, while the other approach advocates the development of stratigraphy consistent with a new biblical geologic timescale.<sup>66,67,75</sup> For information regarding the first approach, review Bartlett<sup>76</sup> and Hunter,<sup>77</sup> and for the second, consult Froede,<sup>78,79</sup> Davison,<sup>42</sup> Reed,<sup>80,81</sup> and Klevberg.<sup>82–84</sup> We encourage more discussion of sequence stratigraphy and its applicability to diluvial geology as it continues to develop within biblical history.

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54. There has long been discussion among young-earth creationists regarding application of the naturalistic geologic timescale to diluvial geology. Unfortunately, it has focused on which ‘parts’ of the timescale are applicable. Conceptually, the naturalistic timescale can be divided into three parts, 1) matching similar sediments (identified as lithostratigraphy), 2) matching similar fossils (i.e. biostratigraphy), and 3) matching similar age-dates, based on radiometric dating (i.e. chronostratigraphy). For those who advocate using a time-compressed naturalistic geologic column, the current idea is to work primarily in the lithostratigraphic framework claiming that the other two corresponding conceptualizations are of less utility (see Snelling *et al.*, ref. 74). While well-intended, the geologic timescale cannot be deconstructed separately because it is a progression of evolutionary and radiometric-derived time assumptions requiring a ‘Precambrian-to-Holocene’ progression, which is unnecessary and, in some cases, counterintuitive to diluvial interpretation. We have proposed a new geologic framework consistent with a scriptural understanding of Earth’s geologic history (see refs. 61, 62, and 68). These two conceptually similar young-earth creationist geologic timescales are incompatible with the naturalistic geologic timescale (see Froede and Akridge, ref. 56).
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59. The ambiguity of how to relate the strict global simultaneity of uniformitarian categories is part of the issue. Perhaps each layer is tied to a single tsunami pulse, such that each megasequence was laid down in the time that it took the tsunami pulse to cross the craton. However, this would have resulted in deposition over wide areas in a matter of hours to tens of hours. However, tsunami-like waves could not have traversed North America for the simple reason that topography and distance would have attenuated them after some discrete distance. Even if this were possible, then things like lithology, fossil content, etc. would be functions of hydrodynamic action, not 'depositional environment' over time. This represents another giant disconnect between biblical and secular geology. Creationists cannot pick and choose which parts of secular geology are applicable until we rethink it from the ground up.
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**John K. Reed** earned B.S., M.S., and Ph.D. degrees in geology. He worked for several decades as a professional geologist in industry and academia. In 1998, John became the geology editor of the *Creation Research Society Quarterly*, and was subsequently elected to the CRS Board of Directors. He has written and edited numerous books and articles about Creation and natural history.

# Evolutionary molecular genetic clocks—a perpetual exercise in futility and failure

Jeffrey P. Tomkins and Jerry Bergman

Since its first use in the early 1960s, molecular genetic clock methodologies assume evolution and deep-time calibrations taken from paleontology. In addition, the following problems plague its use: 1) different genes/sequences give widely different evolutionary rates, 2) different taxa exhibit different rates for homologous sequences, and 3) divergence dates commonly disagree with paleontology despite being calibrated by it. Because the molecular clock idea is directly tied to the neutral model theory of evolution, recent discoveries in full codon utility and pervasive genome-wide biochemical functionality negate its foundational premise.

As stated in a recent review of evolutionary theory: “A molecular clock is now a standard assumption in almost every study of molecular evolution.”<sup>1</sup> The molecular clock has had a major influence in nearly all biological disciplines, as well as causing much grief and dissension for the fields of paleontology and geochronology.<sup>2,3</sup> The basic premise is that informational macromolecules such as proteins and DNA sequences evolve at rates that can be measured and calibrated by evolutionary estimates provided by paleontology.<sup>4,5</sup> The increasing popularity of this methodology, particularly over the past decade, and its use in evolutionary systematics is illustrated by the yearly number of research publications documented in NCBI’s PubMed database (figure 1). While there were only a handful of such papers in the late 1960s and 1970s, current trends indicate that these types of reports may soon top over 100 publications per year.

When the molecular clock was first being developed, much hope was invested in the technique with the idea that it would ultimately allow the construction of a unified evolutionary tree of life marked by historically accurate deep-time points. However, instead of resolving the tree of life, the past five decades of molecular clock research has produced nothing but discordance and confusion within the evolutionary community.<sup>3,6</sup> In fact, in a recent interview this year, human evolutionary geneticist David Reich of Harvard stated: “The fact that the clock is so uncertain is very problematic for us” and “It means that the dates we get out of genetics are really quite embarrassingly bad and uncertain.”<sup>7</sup>

## A history of molecular clocks

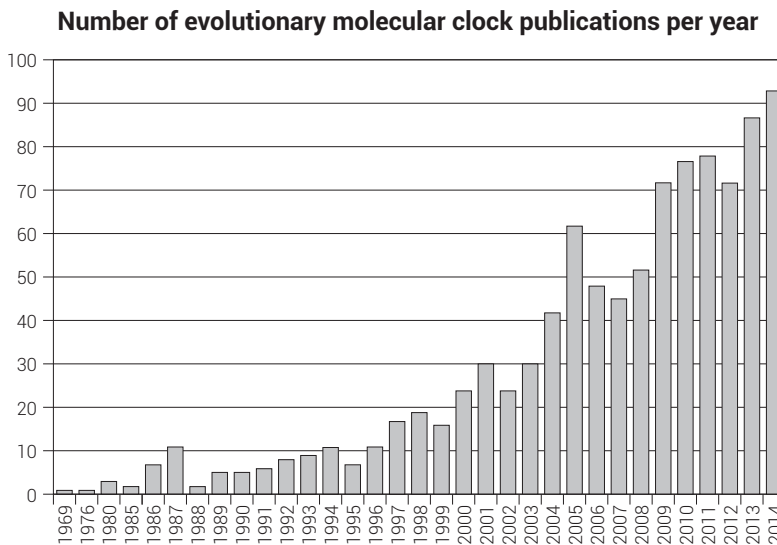
The idea of a molecular clock was first introduced in the early 1960s at a time when molecular biology was still in its infancy and DNA sequencing would not be realized for another decade. According to evolutionary biologist and

historian Sean Carroll, it was Zuckerkandl and Pauling who first proposed a “new picture of evolution that was invisible to paleontologists and taxonomists—a picture of molecules ticking off evolutionary time without affecting how organisms looked, behaved, or functioned.”<sup>8</sup> Zuckerkandl, the post-doctoral scientist of Linus Pauling, stated in an interview 50 years later that “it seemed natural to wonder whether the succession of changes that were obviously taking place through evolution, and not exclusively by any means but to a large extent were then known as attributable primarily to exchanges of individual bases in genes or amino acids in corresponding proteins.”<sup>9</sup>

Zuckerkandl began analyzing enzymatically digested hemoglobin protein fragments from gorillas, chimpanzees, rhesus monkeys, orangutans, cows, pigs, and an assortment of fish.<sup>10</sup> By comparing fragments, he found that human and gorilla globin proteins only differed by one or two amino acids. Using the estimated time of the divergence of horses and humans (taken from paleontology), which they put at 130 Ma, and the number of differences between their  $\alpha$ -chains, they calculated a time of about 14.5 Ma for each amino acid change. Zuckerkandl and Pauling then used this 14.5 Ma value as the standard rate of one change in each alpha globin chain. By multiplying the number of changes by 14.5, then dividing by 2 because the changes occurred across the two lineages, they estimated that the difference between the gorilla and human globin chains indicated their last common ancestor lived from 7.3 to 14.5 Ma ago.

They then averaged these two numbers to obtain 11 Ma, a value that was much earlier than that proposed by paleontologists at the time, which was 11 to 35 Ma. These claims stirred up a heated and contentious controversy with the traditional proponents of the modern Darwinian synthesis of the day. One of the most prominent and vocal skeptics was Ernst Mayr, a leading expert on speciation and systematics, plus George Gaylord Simpson, a prominent





**Figure 1.** Number of publications listed by PubMed at NCBI per year using the combined search terms 'evolutionary' + 'molecular' + 'clock'.

paleontologist. They were two of the chief architects of the so-called Modern Synthesis of evolutionary theory that emerged in the 1940s.<sup>8</sup> Simpson and Mayr inferred from the fossil record that evolution occurred erratically, and some creatures didn't seem to evolve at all. Thus, the idea that it worked like a steadily ticking clock was not readily accepted.

Already, basic presuppositional problems with the molecular clock method should be noted outside of the controversy it caused within the evolutionary community. Namely, it assumes evolution and depends on deep-time calibrations from paleontology.<sup>6,11</sup> As noted, Zuckerkandl and Pauling used the estimated time of divergence of horses and humans to develop their rate of sequence substitution. And as we shall see later, while the statistical applications of this assumption have become increasingly more sophisticated, the basic restraint of evolutionary paleontology has always been a key component of molecular clocks from their first inception.

At about the same time as Zuckerkandl and Pauling's research, immunological techniques (relative differences between taxa in protein precipitate using human antibodies) were also being applied to studying protein relatedness within an evolutionary clock scenario and used for human serum proteins, cytochrome c, and fibrinopeptides.<sup>12–15</sup> However, Zuckerkandl and Pauling strongly pushed the idea of a molecular evolutionary clock based on biological sequence and formalized their ideas further in 1965 stating: "Anyone who recognizes the value of the immunological approach for estimating phyletic distance with certain limits should find it impossible to deny that the comparison of amino acid sequences is potentially an even better tool. It is only potentially less equivocal, more accurate, suited

for absolute instead of only relative evaluations, and able to extrapolate from the present to the past."<sup>16</sup>

While immunological based techniques continued to be applied for a number of years thereafter, the idea of using biological sequences became more important as continuing ideas about selection, neutral changes, and fixation began taking shape in the contentious esoteric cauldron of evolutionary debate at the time. Indeed, some of the first discussions of the idea of the neutral theory of evolution are contained in Zuckerkandl and Pauling's 1965 paper in which they state: "The changes in amino acid sequence, will, however, be limited almost exclusively to the functionally nearly neutral changes."<sup>16</sup> The high

evolutionary rates reported by Zuckerkandl and Pauling along with their ideas about amino acid substitution rates was the first topic addressed in Mootoo Kimura's popular 1968 paper (Kimura was one of the initial key proponents of the neutral theory).<sup>17</sup>

The neutral theory was developed by Kimura in large part as a solution to Haldane's dilemma which Kimura noted by stating: "... the calculation of the cost based on Haldane's formula shows that if new alleles produced by nucleotide replacement are substituted in a population at the rate of one substitution every 2 yr, then the substitutional load becomes so large that no mammalian species could tolerate it."<sup>17</sup> His solution to this problem stated: "the very high rate of nucleotide substitution which I have calculated can only be reconciled with the limit set by the substitutional load by assuming that most mutations produced by nucleotide replacement are almost neutral in natural selection".<sup>17</sup> However, other prominent researchers, who were developing similar ideas at the time (e.g. Jack King and Thomas Jukes), soon noted that Kimura's estimates of per-genome substitution rates could be exaggerated.<sup>18,19</sup> At present, a variety of competing hypothetical evolutionary paradigms exist that propose different levels of neutrality and selection in genome evolution.<sup>20–23</sup>

Nevertheless, the basic idea of the neutral theory provided a strong rationale for the molecular clock, even though the earlier research for a molecular clock slightly predated the formal development and promulgation of neutral theory. The basic model postulates that neutral sites in the genome are not under selection, and that the rate of evolution/substitution at a neutral site is the same as the rate of mutation.<sup>20,24</sup> As we will show later, recent findings of pervasive biochemical

function across the human and other metazoan genomes directly threaten the validity of this concept.

### Rate heterogeneity problems

A major difficulty that evolutionists have had with the clock method is its original assumption that molecules accumulated differences at a regular rate purely as a function of evolutionary time. From the fossil record, paleontologists inferred that the rate of evolution varied greatly, sometimes enormously, while many species remained unchanged for long periods of time (referred to as ‘stasis’).<sup>25</sup> In fact, much to the chagrin of paleontologists, biologists have proposed that the clock hypothesis could even be used for “determining evolutionary events of the remote past for which the fossil and other evidence is lacking or insufficient”.<sup>4</sup>

In the early era of molecular clock research, prior to the genomics revolution, the focus was largely on relatively recent evolutionary events alleged to have occurred during hominid evolution.<sup>12,13,26</sup> As the DNA sequencing advanced, more ambitious efforts to ascertain divergence dates among diverse animal phyla and even for the major kingdoms of living organisms was undertaken.<sup>27,28</sup> However, it soon became apparent that wide rate differences existed between phylogenies based on genetic analyses and those obtained strictly by the fossil record. As noted by Ho *et al.*: “Rates of microevolutionary change [within species], measured between successive generations, were found to be far higher than rates of macroevolutionary change inferred from the fossil record.”<sup>29</sup> Venkatesh *et al.* concluded that analyses “of molecular sequences have given conflicting models even when large data sets were used”.<sup>30</sup>

The most empirical way to measure genetic change is by determining DNA base substitutions observed between generations of pedigree lines. These have been shown to greatly exceed the more speculative and spurious rates achieved from paleontology.<sup>6</sup> Some researchers have attempted to correct this conflicting empirical data with the hypothetical effects of selection.<sup>31</sup> The other method of determining genetic change is purely hypothetical and based on comparing homologous sequences between diverse taxa. This could be called the phylogenetic method, while the former could be termed the biochemical method. When either method is used, the data is typically calibrated with deep time.

With either method of determining the genetic clock rate, the prospects of achieving any type of evolutionary concordance has been dismal. As noted in a recent review, the author stated that the estimation of divergence dates “is a perilous exercise fraught by artifacts which become progressively more severe for events further in the past” and, “These difficulties are intrinsic to the dating of ancient

divergence events and are reflected in the large discrepancies between estimates obtained with different approaches.”<sup>32</sup>

Alongside the progression of such studies over the years, has been the growing recognition that rate variation (also termed rate heterogeneity) contradicted the foundational premise of the molecular clock. To combat this enigma, analyses now include sophisticated models that incorporate rate heterogeneity across the different lineages.<sup>33</sup> However, rate variation is an important evolution-negating problem that cannot simply be swept under the rug with sophisticated statistical models. It must be fully understood to appreciate the deep fundamental problems that exist in evolutionary molecular clock research.

The underlying components of rate variation are multifactorial and include gene sequence effects, lineage effects, and residual effects (the difference between the observed value and the *estimated/predicted* value).<sup>34</sup> For the purposes of this study we will focus on gene and lineage effects since the large levels of residuals common to such studies are largely the result of the inconvenient fact that the data by its nature contains many statistical outliers, primarily because evolutionary assumptions don’t fit real world biology.

The influence of gene or genomic region effects are notorious and plague nearly all studies done in molecular clocks.<sup>34</sup> This inconvenient fact was widely popularized by evolutionist Francisco Ayala at the beginning of the genomics revolution when he noted “... every one of the thousands of proteins or genes of an organism is an independent clock, each ticking at a different rate”.<sup>35</sup> In illustrating this concept, Ayala noted the glaring example of molecular clock disparity for the superoxide dismutase (SOD) and glycerol-3-phosphate dehydrogenase (GPDH) genes that encode key metabolic proteins found in a diversity of animals. In regards to these genes, Ayala states: “*Drosophila* flies and mammals (which have longer generation time and lesser population numbers than occur in *Drosophila*) evolve at the same SOD rate, but mammals evolve five times faster in the case of GPDH.” He then notes that one of the key problems with this discrepancy is that the “intra-cellular role of scavenging oxygen radicals would seem likely to have remained the same through time and across lineages over the last 650 My [Ma]”. His conclusion is “that we are left with no predictive power and no clock proper”.

Another significant problem is that while some genes differ widely in their sequence characteristics, others exhibit little change across a wide variety of life forms. For this reason, histone genes are never used because they would generate a molecular clock and divergence dates in complete contradiction to those obtained from studies of other less conserved genes.<sup>36</sup> In another of many examples, the motor protein myosin 2 is structurally identical in turkeys and

scallops despite the 600 Ma of evolution that separates the two life forms.<sup>37</sup>

In a recent study among primates evaluating differences in conserved CpG islands across the genome, Kim *et al.* reported: “Our conclusion that different regions of genomes follow different molecular clocks should be considered when inferring divergence times using molecular data and in phylogenetic analysis.”<sup>38</sup> They also determined that heterogeneous genomic molecular clock sites across the different primate genomes were of a “markedly different nature, reflecting differences in their molecular origins”. Even more remarkably, the authors showed that two different types of genomic clocks operated in these regions in which they “demonstrate that the two types of mutations [replication origin and methylation origin] follow statistically different molecular clocks”. They go on to say: “Methylation-origin mutations accumulate relatively constantly over time, while replication-origin mutations scale with generation-times.”

Rate variations exist not only for different genes and genomic regions, but also among lineages, including major metazoan ones. Peterson *et al.* pointed out this discrepancy, stating that “comparative genomic analyses suggest that a significant rate difference exists between vertebrates and dipterans, because the percentage difference between the genomes of mosquito and fly is greater than between fish and mouse, even though the vertebrate divergence is almost twice that of the dipteran.”<sup>39</sup> As an author of one evolutionary review paper stated: “Differences in the rate of evolution across the major groups of life are dramatic.”<sup>40</sup>

Even within a more restricted group of organisms that have somewhat similar molecular machinery, such as mammals, rate variation among taxa can be large. The most popularized of these is the discrepancy between rodents (murid rodents in particular) which have an elevated substitution rate compared to apes and humans, which have a decreased rate.<sup>41</sup> This has been famously termed “the hominid slowdown” by evolutionists. Interestingly, in an even more restricted sense, just among different bat taxa, rates were also found to vary widely.<sup>40</sup>

So what is the biochemical cause of this rate variation among different animal taxa? The level of discrepancy in the dating of a single set of organisms caused by lineage effects can often be as high as twenty-fold.<sup>42</sup> While many factors contribute to it, an evolutionary answer has been elusive. In a comprehensive study that analyzed mutation rates in a diverse set of 44 homologous genes for 2,108 nodes on the mammalian super-tree, the researchers stated: “Despite concerted effort, the reasons underlying any global lineage-specific differences remain unclear, with explanations invoking or refuting any, or all, of the differences in cellular DNA proofreading and repair mechanisms, body size, mass-specific metabolic rate, and/or (genomic) generation time.”<sup>40</sup>

## Codons—not so redundant after all

In the protein coding regions of genes, three consecutive DNA letters form what is called a codon, and each codon corresponds to a specific amino acid in a translated protein. An early noticed aspect of codons is that of apparent redundancy where the first two bases are non-negotiable, but the third base can vary. The variation in the third base was termed ‘wobble’ and codon variability was considered redundant. In effect, it was assumed that different codon variants for a given amino acid were functionally equivalent.

When alleged codon redundancy was discovered, scientists were interested in the possible evolutionary role that mutations in the third base might play.<sup>43</sup> In the emerging dogma of the day, mutations that did not alter the encoded amino acid of a codon (synonymous) would ultimately have no effect on the resulting protein sequence and thus, have no effect on cellular functionality, organismal fitness, or selective evolutionary processes. They were ideal candidates for neutral sites of evolution.

Neutral model proponent Masatoshi Nei stated in 2005: “Because of degeneracy of the genetic code, a certain proportion of nucleotide substitutions in protein-coding genes are expected to be silent and result in no amino acid substitution.”<sup>21</sup> Nei *et al.* re-affirmed this widely held belief in a 2010 paper followed by his book, *Mutation Driven Evolution*, published in 2013.<sup>22,23</sup> However, in recent years, evidence for multi-role functionality at the codon’s third position has been rapidly mounting.

Organisms across the spectrum of life show large variability in their particular preferences for the use of different codons that encode the same amino acid.<sup>44–46</sup> In one interesting study, 50 randomly selected genes were chosen from four diverse prokaryotes and five diverse eukaryotes (including humans) and the level of codon preference was found to not only vary among taxa, but also vary widely between genes even within an organism’s own genome.<sup>44</sup> This intra-genome variation for codon preference was more recently confirmed in an extensive study among insect taxa.<sup>46</sup> As noted in a recent review of the subject, such complicated scenarios of codon usage represent “features that are difficult to explain through mutation alone”.<sup>44</sup>

Early on it was known that changes in the third base of codons do affect the functional effectiveness of the cell because of the enormous interconnectivity of cellular biochemistry. An example is that a specific codon code is tied to the tRNA production system, and a change in a codon thus impinges upon the effectiveness of the protein translation apparatus. The tRNA production levels are ‘set’ for the original code, and changes cause a tRNA supply imbalance.<sup>47</sup> More recently, it was discovered that tRNAs are re-used in the translation process and that codon sequence, especially



at the third base, plays a large role in this recycling system.<sup>48</sup> This is especially true for genes that are highly and rapidly expressed to improve translation efficiency.

One of the largest problems for the idea of redundancy, however, has been the discovery in recent years of dual codes found in codons. In complex eukaryotic genomes, it has been widely demonstrated that protein-coding exons contain a variety of signals (e.g. splice sites, editing sites, miRNA binding sites, mRNA turnover signals, etc) other than just the information delineating amino acids.<sup>49</sup> It was also recently demonstrated in a genome-wide study in humans that transcription factors commonly clamp onto specific sites encoded within exons inside genes.<sup>50</sup> While one set of codons specifies the order of amino acids for a protein, the very same sequence specifies where transcription factors are to bind to regulate transcription.<sup>51</sup> More specifically, it was determined that about 14% of the codons inside 87% of human genes are occupied target sites for transcription factors. These dual-function codon sites in exons have been labeled 'duons'.

The evolutionary implications for the preponderance of dual codes in codons, particularly as it relates to the neutral model, immediately became obvious to the scientific community. Several researchers in a recent review recognized this problem and stated: "How widespread is the phenomenon of 'regulatory' codes that overlap the genetic code, and how do they constrain the evolution of protein sequences?"<sup>52</sup>

In addition to the discovery of duons, it has also been recently documented that the third base of the codon plays a key biochemical role during protein translation. During translation, periodic pausing occurs while the protein is being produced and directed out of a tunnel in the ribosome.<sup>53,54</sup> The sequence specified in codons affects the rate of pausing in the ribosome, and is critical to the folding of proteins into their proper three-dimensional shape which occurs during the process of exiting the ribosome. Because the translation and the initial folding of the protein are linked together, the processes are called 'co-translational'. A recent study has shown that the third base is key to telling the ribosome when to pause and how to regulate the rate at which the protein is being made, which ultimately determines the folding of the protein into its proper three-dimensional shape.<sup>55</sup> Not only does a codon provide the alphabet for which amino acid to add in a protein, but it provides important information needed to regulate its folding. The researchers state: "These dual interpretations enable the assembly of the protein's primary structure while also providing important folding controls via pausing of the translation process."

What was once thought only to be meaningless redundancy and fodder for neutrally evolving sequence, has now been proven to be exactly the opposite. Clearly

codons are information rich features containing multiple overlaying languages and sets of instructions for different systems in different parts of the cell. In fact, the researchers of the most recent protein folding study go on to say: "The functionality of codonic redundancy denies the ill-advised label of 'degeneracy'."<sup>55</sup> They add: "Redundancy in the primary genetic code allows for additional independent codes. Coupled with the appropriate interpreters and algorithmic processors, multiple dimensions of meaning and function can be instantiated into the same codon string."<sup>55</sup>

### Genes are networked

Another problem with the molecular clock is that genes do not function as single entities, but rather are part of complex, highly interconnected genomic networks. This concept was recently demonstrated when scientists observed the effects of 550 sequentially inhibited genes on the overall fitness of nematodes over eight generations.<sup>56</sup> Fitness is defined here as the ability of a population of organisms to grow and reproduce over time compared to a control population that did not have the mutation. In the majority of cases, the disruption of single genes reduced the fitness of the nematode populations. This was an effect that kept increasing with successive generations. Theoretically, this would have eventually led to extinction. As a result, the researchers concluded that almost every gene tested was essential to survival of the nematode. And because the mutant worms' fitness decreased over successive generations, the researchers also concluded that even single mutations negatively impact entire gene networks. The researchers wrote: "In contrast to previous estimates, we find that, in these multigeneration population assays, the majority of genes affect fitness, and this suggests that genetic networks are not robust to mutation. Our results demonstrate that, in a single environmental condition, most animal genes play essential roles."

Compounding the evolutionary problem of interconnected genes is the fact that the boundaries of what constitutes a gene have become blurred as we begin to unravel the complexities of the genome. What was once thought to be a single gene can instead be a nest of different genes due to the fact that introns can contain genes, genes can overlap, and many genes have antisense counterpart genes located on the opposing strand.<sup>57-60</sup> Also, regulatory sequences such as promoters and enhancers that can control and regulate several genes (even bi-directionally), can be located at long distances away from the genes they control (up to a million bases), or even be found inside neighbouring genes, and are themselves often transcribed to produce products that participate in gene regulation and/or chromatin modification.<sup>61-64</sup> In addition to protein coding genes, it is now widely understood that up to twice as many long noncoding RNA genes exist in the

genome that are coregulated and networked with protein coding genes.<sup>65–69</sup>

Taking into account this level of interaction and complexity and applying it to standard evolutionary clock analyses is essentially beyond reason at this point. One of the leading researchers attempting to do so has been Michael Lynch. In his view, “Although numerous investigators assume that the global features of genetic networks are moulded by natural selection, there has been no formal demonstration of the adaptive origin of any genetic network” and “the mechanisms by which genetic networks become established evolutionarily are far from clear”.<sup>70</sup> So what sort of model does Lynch propose to explain the origination of complex genetic networks? Something akin to the neutral mutation-driven model on a grand scale where genomes just somehow mystically evolve through random genetic drift. He states: “... many of the qualitative features of known transcriptional networks can arise readily through the non-adaptive processes of genetic drift, mutation and recombination, raising questions about whether natural selection is necessary or even sufficient for the origin of many aspects of gene-network topologies.”

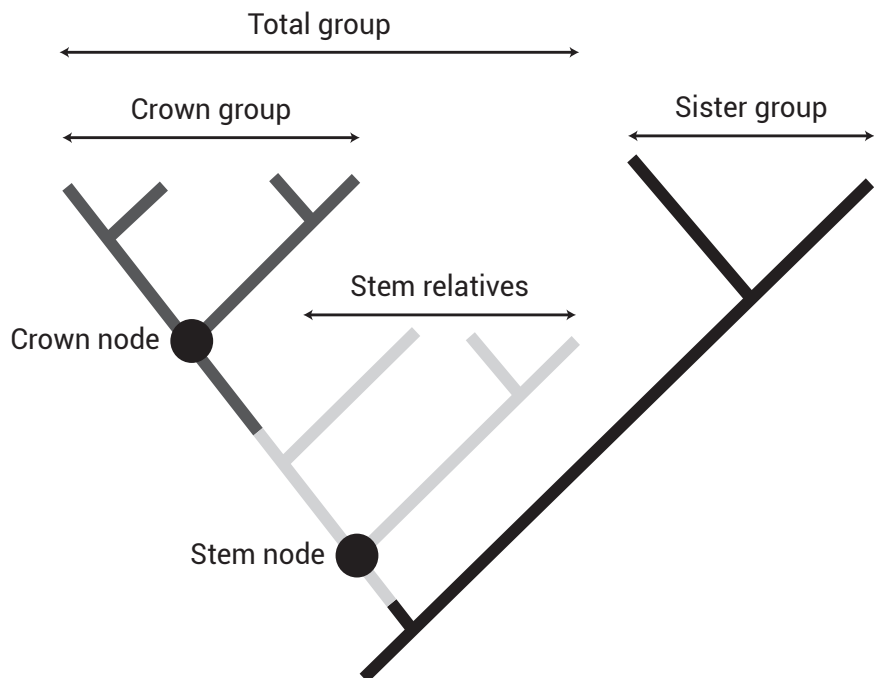
Interestingly, several years after Lynch published this hypothetical paper, he produced several other papers showing how random mutation on a genomic scale was actually counterproductive to evolution. One paper described an extensive population genetics study in water fleas, a complex eukaryote, and found that genetic lines with high germline spontaneous mutation rates generally had lower levels of fitness.<sup>71</sup> Thus, an increase in spontaneous mutation rate, the alleged engine of evolution, actually lowered the ability of the organism to both survive and reproduce. Another report by Lynch showed how the organismal mutation rate decreases with both genome size and effective population size among both prokaryotes and eukaryotes.<sup>72</sup> And yet another report showed that while the total amount of transposable elements, intron size, and other noncoding DNA—alleged candidate regions for neutral model evolution—all increased with genome size, the recombination rate decreased.<sup>73</sup>

So if the amount of alleged junk DNA is increasing with genome size, the fodder of neutral model evolution, why is the mutation rate not scaling accordingly? Clearly, the answer is that nearly all of the genome is serving some undiscovered functional purpose, even in those genes that appear to be extensively populated with retroelements as is often observed in many plant species.

Complex, genome-wide, biochemical functionality following multiple lines of combinatorial evidence associated with pervasive transcription, long noncoding RNA functionality, complex patterns of chromatin modification, and genome-wide co-regulation data, is now being widely documented in both plants and animals.<sup>63,69,74–79</sup> Thus, the amount of genomic landscape not under functional selective constraint (as the evolutionist would view it) is diminishing rapidly as research progresses.

### Molecular clock discrepancies with paleontology

In a recent paper, the authors state: “Major disparities are recognized between molecular divergence dates and fossil ages for critical nodes in the Tree of Life.”<sup>80</sup> In this same paper the authors specifically documented huge disparities between paleontology and molecular clock dates for 67



**Figure 2.** Basic evolutionary terminology of inferred phylogenetic relationships used in calibrating and developing models for molecular clocks. A crown group is the most recent common ancestor located at the crown node of a living clade, which would also include all the living and extinct descendants of that ancestor. A stem node represents the inferred evolutionary divergence of all members of a monophyletic group descended from a common ancestor, including extinct lineages alleged to have diverged below crown groups, called stem relatives.

clades of birds. They found that “for Aves, discord between molecular divergence estimates and the fossil record is pervasive across clades and of consistently higher magnitude for younger clades” and “These divergence estimates were, on average, over twice the age of the oldest fossil in these clades.”

In another very recent and an even more taxonomically broad study among placental mammals, researchers examined a complex matrix of morphological characters in combination with a large nuclear DNA sequence dataset and total discordance with the fossil record was the end result.<sup>81</sup> These conflicting results were accomplished despite the fact that two very different relaxed clock models were used to account for extensive rate heterogeneity, including one that was constrained using the current evolutionary consensus for placental phylogeny. The authors stated that the end result of the effort was to “retrieve implausibly ancient, Late Jurassic–Early Cretaceous estimates for the initial diversification of Placentalia (crown-group Eutheria)” and that “These dates are much older than all recent molecular and palaeontological estimates.” To try and force their results to fit the evolutionary paradigm, they added even stronger deep-time constraints and stated: “Enforcing additional age constraints on selected internal divergences results in only a slight reduction of the age of Placentalia.”

The frustration that this common discrepancy has caused the evolutionary community was recently voiced in a paper written by paleontologists in which the authors stated:

“As paleontologists who frequently collaborate with geochronologists, we expect that molecular ‘timetrees’

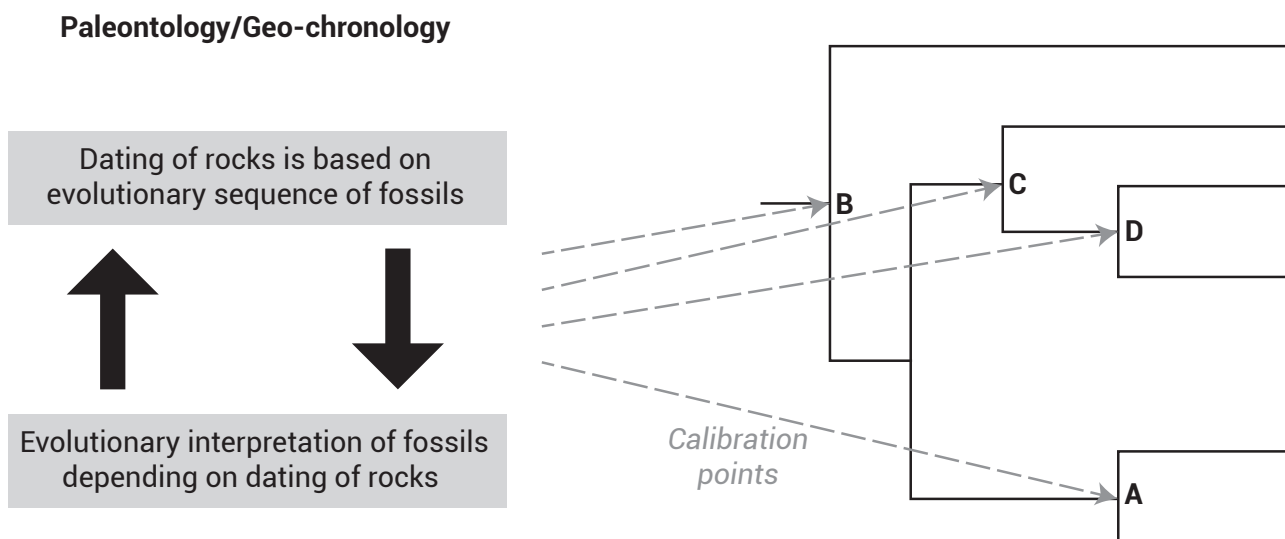
will help fill gaps in the fossil record. However, we find molecular divergence-age estimates (‘dates’) difficult to evaluate, and not only because many results differ strikingly from the fossil data. Molecular dates are extremely sensitive to placements of calibrating fossils at stem vs crown nodes and to choices of methods and calibration scenarios.”<sup>83</sup>

Figure 2, in addition to illustrating the concept of evolutionary phylogeny, depicts the difference between stem and crown nodes.

Interestingly, this discrepancy between the two dating systems (genetic vs paleontology) has led some biologists to propose the idea that somehow molecular clock rates not only vary between genes and lineages, but that they must also vary across deep evolutionary timescales.<sup>82</sup> Because the two systems (genetic clocks and paleontology) do not consistently agree with each other, this brings us to the main issue of molecular clock theory—calibration and the overriding assumption of evolution.

### Clock calibration—the crux of the matter

When evolutionists ascertain time in a phylogenetic tree, they routinely insist that “the molecular clock needs to be calibrated”.<sup>34</sup> In other words, clock calibration is standard operating procedure and is based on the presupposition of evolution and deep time, and has been implemented since the first studies published by Zuckerkandl and Pauling. However, as noted in a recent review, “uncertainty in the fossil or geological information used to construct calibrations is



**Figure 3.** Basic illustration of the circular reasoning employed in paleontology and the points (nodes) in an evolutionary phylogeny to which they are employed. Possible points of calibration and constraint according to guidelines at [timetree.org](http://timetree.org) could include a minimum constraint (hard bound) that would be the oldest fossil in a group or a maximum constraint that could be a probability distribution of the fossiliferous rocks related to the time in question.



rarely trivial”.<sup>34</sup> Of course, creationists have long pointed out the serious problems with using fossils and geochronologic dating systems, unequivocally showing that they cannot be used as a valid basis of ancient time determination or as proof for macroevolution in a cohesive tree-of-life continuum.<sup>83–88</sup>

As stated in a recent evolutionary review: “In all molecular-dating analyses, the single most important component is the choice of calibrations.”<sup>89</sup> Molecular clock calibration is generally accomplished in one of two ways: by setting the rate to an alleged known value taken from paleontology or by constraining the age at one or more nodes in the phylogeny using the alleged age of fossils and/or a hypothetical geochronologic event.<sup>6,34,90</sup> See figures 2 and 3, which show the various types of points (nodes) in a phylogenetic tree that are ‘calibrated’ by evolutionary assumptions. Because agreeable rate estimates are typically hard to come by, the latter approach is usually employed when many diverse taxon are used over a large amount of evolutionary time, particularly when there are substantial rate differences among the lineages—a pervasive anomaly described earlier.

Typically, the earliest fossil in a lineage is used to infer time of divergence for that lineage from its alleged sister lineage.<sup>91</sup> The supposed age constraint can be applied in several ways, of which the easiest is to fix the node’s age to a single point value. Of course, this methodology ignores the inherent uncertainty in the evolutionary-based calibration of the geochronologic age(s) associated with both radiometric dating and taxonomic assignment. Thus, many studies attempt to account for this uncertainty by allowing the age of the phylogenetic node to vary within chosen limits.<sup>6,34</sup>

A survey of deep-divergence studies by molecular evolutionists Dan Graur and William Martin critiqued one particular study in which the authors “claim to be 95 percent certain that their divergence date for certain animal groups falls within a 14.2-billion-year range—more than three times the age of the earth and a clearly meaningless result”.<sup>5</sup> Graur and Martin further document the absurdity of the problem by stating that these scientists “inferred ostensibly precise molecular-clock dates for speciation events ranging from the divergence between cats and dogs to the early diversification of prokaryotes”. As Graur and Martin noted, divergence-time estimates are often based on a single calibration point and tenuous methodology stating that the “calibration point that is both inaccurate and inexact—and in many instances inapplicable and irrelevant—has been used to produce an exhaustive evolutionary timeline that is enticing but totally imaginary”. They concluded that many molecular clock estimates “look deceptively precise” but, given the many problems with this technique, their “advice to the reader is: whenever you see a time estimate in the evolutionary literature, demand uncertainty!”

However, despite the inherent evolutionary uncertainties associated with calibrating the molecular clock, the overriding problem is the illogical circular reasoning surrounding the whole process (figure 3). Molecular genetic clocks are calibrated by fossils that are themselves calibrated by their sedimentary rock formations and the sedimentary rock formations are calibrated by the fossils. Ultimately, the presupposition and assumption of evolution is the overriding paradigm—calibrating everything. Even honest evolutionists will occasionally admit to this, as explained by Schwartz and Maresca in their 2007 paper titled: “Do molecular clocks run at all? A critique of molecular systematics”.<sup>92</sup>

“Although molecular systematists may use the terminology of cladism, claiming that the reconstruction of phylogenetic relationships is based on shared derived states (synapomorphies), the latter is not the case. Rather, molecular systematics is (largely) based on the assumption, first clearly articulated by Zuckerkandl and Pauling (1962), that degree of overall similarity reflects degree of relatedness. This *assumption* derives from interpreting molecular similarity (or dissimilarity) between taxa *in the context of a Darwinian model of continual and gradual change* [emphasis added].”

## Summary

The paradigm of an evolutionary molecular genetic clock employs the multiple alignment of biological sequences combined with a variety of sophisticated statistical models to estimate rates of evolution among diverse taxa that creationists would consider to be completely separate created kinds. Since its first inception and use in the early 1960s, standard molecular clock methodologies routinely use deep-time calibrations taken from paleontology and assume macroevolution based on a grand tree of life. In addition to this presuppositional bias, the following problems still plague the use of the molecular clock: 1) different genes/sequences give widely different evolutionary rates (even among genes within the same genome); 2) different taxa exhibit widely different rates of change for seemingly homologous sequences; and 3) clock-derived divergence dates commonly disagree with paleontology despite the fact that deep-time calibrations are incorporated into the evolutionary clock models. Furthermore, because the molecular clock idea is directly tied to the neutral model theory of evolution, recent discoveries in full codon utility and pervasive genome-wide biochemical functionality, present serious obstacles to the evolutionary necessity of a large fraction of the genome being ‘junk’.

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# Finally setting the record straight—Christian views on the historicity of Adam through the ages

***The Quest for the Historical Adam: Genesis, Hermeneutics, and Human Origins***

William VanDoodewaard

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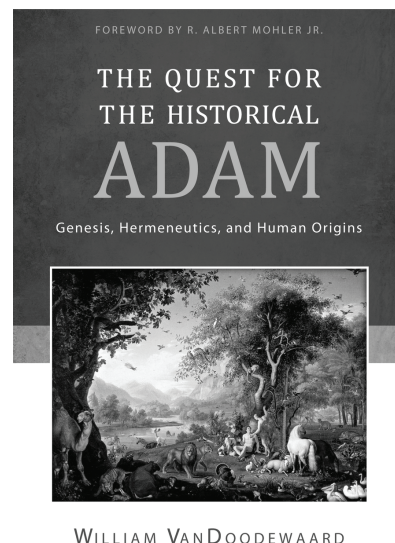
Robert Carter

Dr William VanDoodewaard is Professor of Church History at Puritan Reformed Theological Seminary. Even though his book is focused on theological arguments within Reformed circles, there is plenty of good material here for Christians in general. Not only does it deal fairly with both sides on this complex topic, but it does so comprehensively. The creation-evolution argument is not new. It has been part of church history, under shifting definitions, from the very beginning, but only a few are aware of this. I am keenly interested in church history, but not being a specialist there are many aspects that I have not had time to delve deeply into. This is also interesting to me for the fact that I was once publicly stumped during a radio interview on a show with a Reformed Presbyterian host. A caller made the comment that he understood what I was trying to say (concerning the reality of Adam and Eve) but wondered why no Reformed scholar of any repute agreed with me. Then, starting with Charles Hodge and B.B. Warfield, he rattled a list of about 15 scholars, all of whom I was familiar with, to make his point. I had little to say, but

did counter with “R.C. Sproul”, for during a short window of time Sproul seemed to be on our side. My mistake was that I did not reach to a time *before* Hodge and Warfield, for then I could have called on almost every scholar in their tradition. VanDoodewaard has helped me to understand this much more clearly.<sup>1</sup> For modern scholars, we have David Hall and Joseph Pipa, for example, but these able men are, to date, less well known than some of the larger figures in history, and I was unable at that time to vocalize their names when put on the spot.

To be fair, the book is about the debate in *theological* circles. Thus, there is scant mention of mainstream creationists. Likewise, and even though theology and science have overlapped considerably over the centuries, scientists who have supported the Creation account of Genesis are barely present. Yet, by filling in a giant historical gap, we can lay to rest any notion that ‘creationism’ is a modern theological innovation, and certainly does not begin with the Seventh Day Adventist, George McCready Price (1870–1963), as Ronald Numbers, a professor of the history of science, impotently tried to argue.<sup>2</sup>

And yet, we must be careful to define terms and to carefully parse the various arguments. The age of the earth, the time required for God to create, and the historical reality of Adam and Eve are separate questions. Various people have held different views on these three ideas over the centuries. Nearly all major scholars in the Reformed tradition have believed in a real Adam and Eve. On the other



hand, most of the early ones, but not most of the latter ones, also believed in a young Earth. There is certainly a ‘slippery slope’ involved in allowing secular philosophy to influence biblical interpretation, and that is amply documented in this book, but this does not mean that all scholarship has always had unanimous agreement on the big questions.

He begins with a survey of the relevant passages of the Old and New Testaments, then divides his discussion into time periods: Patristic, Medieval, Reformation, Post-Reformation, Enlightenment, 19<sup>th</sup> Century, Early 20<sup>th</sup> Century, and 1950s to present (this is my division and it does not necessarily correspond to chapter headings).

## The Patristic and Medieval eras

Throughout this historical survey, VanDoodewaard attempts to make the case that the similar arguments have been made for two millennia, with the same counter arguments. Starting with Philo of Alexandria (20 BC–AD 50), a Hellenized Jew who interpreted Genesis allegorically, he notes that Christian scholarship in that same city, notably Clement of Alexandria (c. 150–210) and his successor, Origen (c. 184–254), followed similar paths.

He adds to that list Augustine of Hippo (354–430) and Thomas Aquinas (1225–1274). There is some difficulty with this, however, and it may be that VanDoodewaard is jettisoning some scholarship too quickly. Specifically, Zuiddam<sup>3</sup> and Sibley<sup>4</sup> both make the case that, although some early people allegorized Genesis, this does not necessarily mean they thought it was not historical *at the same time*. Of course, allegorization laid the groundwork for further departures in the future, but not every scholar who leaned that way was on the edge of apostasy, and Aquinas apparently accepted the fact of a 6-day Creation Week.

Yet, the debatable positions of these scholars represent minor positions, and this is critically important. For example, contemporaneous with these were the author of 1 Clement (c. 90–100), Justin Martyr (100–c.165), Theophilus of Antioch (died c. 183–185), Basil of Caesarea (329–379), and Nicholas of Lyra (c. 1270–1349), who clearly took Genesis in the ‘literal’ sense.<sup>5</sup> Many scholars are mentioned in each time period, some lesser known and some well known to us today. However, by citing many contemporaries of the more famous writers, he ably makes the case that, at least until very late in the Christian era, a strong majority of writers accepted, and defended, a straightforward reading of the Genesis text. Also, it appears that each time the allegorical hermeneutic was attempted, it was an attempt to harmonize Scripture with Greek natural philosophy. And, it should be noted that the early allegorists were not trying to *lengthen* the duration of creation. The opposite, in fact, was true—they proposed that God created in an *instant*. Yet, by allegorizing the Creation passages, they paved the way for later dismissals of the historical reality of those passages.

The Medieval period saw similar arguments to those found in the Patristic and early-church era, with notable figures like ‘the venerable’ Bede (c. 673–675), Anselm of Canterbury

(c. 1033–1109), and Peter Lombard (c. 1100–1161) ably arguing for the traditional sense and standing against the minority position of the likes of Irish monk Johannes Scotus Eriugena (c. 815–877), and others. Anselm noted that the Augustinian allegorical view, that God would have created all things in an instant, was common in his day, but this is not borne out by comparison to the writings of the majority of his contemporaries. There is also a parallel in Medieval Jewish scholarship, with a literalist majority arguing against the allegorical minority, e.g. Maimonides (1135–1204) who was influenced by Aristotle (367–347 BC).

### The Reformation

The Reformation saw a strong and nearly unanimous appeal to the plain sense of the Scriptures. William Tyndale (c. 1492–1536) strongly rejected the late Medieval tendency toward allegorization, while at the same time anticipating the modern concept of assessing individual passages in their proper historical-grammatical context and the idea that Scripture should be used to interpret Scripture. Martin Luther (1483–1546) came out strongly in favour of the traditional, literal view. Indeed, Luther seems to be the harbinger of a nearly unanimous view among Reformation and Post-Reformation scholars, including Philip Melancthon (1497–1560), Huldrych Zwingli (1484–1531), and John Calvin (1509–1564). Heinrich Bullinger (1504–1575) wrote clearly about the creation of Adam and Eve in his *Decades*, a work popular among later English scholars.

One less well known but interesting scholar was Lambert Daneau (c. 1530–1595), a student of Calvin. Daneau attempted to create a Christian natural philosophy, using what would later be called “Mosaic physics” and appealing to the Bible for scientific insight. He seems to presage the modern creationist movement. John Woodward (1665–1728), an Englishman living in the time of Newton and writing

contrary to Newton’s views on the age of the earth, would follow a similar line of thought, using his great collection and general knowledge of fossils to support global Flood theory.

Westminster scholar John Lightfoot (1602–1675) and his slightly more famous contemporary James Usher (1581–1656) both wrote extensively on these issues, supporting the literal sense of the Creation account. John Owen (1616–1683) and Thomas Manton (1620–1677) represented the next generation of scholars following this trend. According to VanDoodewaard, the post-Reformation scholars represented by the English Puritans and Dutch Reformed movements held a strong commitment to the literal tradition. Figurative interpretations were more common among the Roman Catholics and smaller splinter groups. Should it surprise anyone that the Catholic Church, in general, seems to have little problem with evolutionary theory?

From the historical records, it is clear that most influences pulling scholars away from the straightforward hermeneutic were coming from outside the church, and these influences were both philosophical and scientific. Yet, these are really just two ends of a continuous spectrum and both always at least minor in the other, but earlier arguments were *more* philosophical and modern arguments are *more* scientific.

It was a little surprising to me to realize that modern attempts at re-writing Genesis have strong parallels in earlier eras. For example, building on Augustine, Medieval astronomer and pioneer of optics, Robert Grosseteste (c. 1168–1253), Bishop of Lincoln, essentially anticipates Meredith Kline’s (1922–2007) Framework Hypothesis, which removed any meaningful correspondence to chronology. There are also many examples of teacher-student pairs where the student takes the arguments one logical step further than his teacher was willing to go.





Figure 1. Adam, Eve, and the Serpent at the entrance to Notre Dame Cathedral in Paris.

### Post-Reformation challenges

About the same time Europeans began the Age of Exploration, new theologies began to pop up. Specifically, pre-Adamite theory, which had no precedent in Christian theology. Philip von Hohenheim (1493–1541) said Africans might lack souls and thus might not be human. This was restated in different ways by several others but remained a minority position until the time of Isaac La Peyrère (1596–1676). He concluded that only Jews were descended from Adam, that the world was lawless but sinless before Adam, and that the Flood had to be local. His rejection of biblical inspiration was similar to that of Thomas Hobbes (1588–1679) and Baruch Spinoza (1633–1677). However, there was a significant reaction to La Peyrère among Reformed scholars, notably from the pen of Francis Turretin (1623–1687). Modern creationists will recognize the major proof texts used by Turretin (e.g. Exodus 20:8–11, Isaiah 54:9, Mark 10:6,

and Romans 5:12–21), as well as his main arguments used in defence of the Bible. The influential lawyer-turned-uniformitarian-geologist Charles Lyell (1797–1875) also taught pre-Adamite theory, and his contemporary, Louis Agassiz (1807–1873), believed in the multiple origin of humans. The Presbyterian minister, more famous for his post-Civil War defence of slavery, Robert Louis Dabney (1820–1898) held his ground, understanding that, “If there are men on earth not descended from Adam’s race, then their federal connection with him is broken.”

The Scottish Reformed church, the English Puritans, the Dutch Reformed, and the Lutherans each kept a strong literal tradition, especially compared to the Anglicans and Roman Catholics. The *Annotations on the Whole Bible ordered by the Synod of Dort* (1637) and the *Westminster Confession* (1653) came down strongly on creation issues. He did not mention it, but the *Second London Baptist Confession of Faith* (1689) did as well, amplifying and

clarifying a brief statement about the creation of man made in the 1646 version. But the *Thirty-Nine Articles* of the Church of England (1563) did not even mention creation. Thomas Burnet (1635–1715) was an Anglican and at one point a tutor to William III. He wrote, troublingly, “‘tis a dangerous thing to engage the authority of Scripture in disputes about the natural world, *in opposition to reason*”, that Genesis is only describing the age of the *earth*, that those who believed in a young universe were doing “violence to the laws of nature”, and that Moses was not trying to describe the beginning of the world “according to the *physical* truth” [emphasis mine]. His separating of the Bible’s spiritual claims from the physical claims of science should seem familiar to the student of the modern evolution-creation debate. In a similar vein, Isaac Newton (1642–1727) wrote: “[The] distinction of the six days in the Mosaical formation of the world is no physical reality.” Newton’s successor, William Whiston (1667–1752), also a famous translator of Josephus, believed there was much time *prior* to Adam and Eve. Yet, among the “non-conformists”, including Matthew Henry (1662–1714), John Gill (1696–1771), and nearly the entirety of the Scottish Presbyterians, we see clear and unambiguous support for the orthodox view of creation. Among the descendants of the Puritans in North America, Cotton Mather (1663–1728) was somewhat ambiguous, but not about his opposition to pre-Adamite theory, while during the Great Awakening Jonathan Edwards (1703–1758) was ambiguous about nothing.

At this same time, however, the anti-Christians François-Marie Arouet, aka Voltaire (1694–1778), David Hume (1711–1776), Immanuel Kant (1724–1804), and others were writing influential works that were shaping intelligent debate. Hume included pre-Adamite ideas. It is interesting to note the intersection of the ‘Enlightenment’ with the obvious and detrimental effects of racism, especially scientific



racism and how the children of the Enlightenment have attempted to tar Bible believers with the outcome. George-Louis Leclerc, Comte de Buffon (1707–1788) was widely influential in pushing what we now call “naturalism”, and his successor, Jean-Baptist Lamarck (1744–1829), added early evolutionary ideas. James Hutton (1726–1797) added long ages of geology to the mix to complete the cycle. Charles Darwin (1809–1882) and his evolutionary biology was supported by the now-discredited but then-popular writings of Ernst Haeckel (1834–1919), who detested the Bible for teaching racial equality,<sup>6</sup> among other things, Darwin’s cousin Francis Galton (1822–1911) was pushing evolution-based ‘eugenics’ theory, and Eugene Dubois (1858–1940) was promoting fossils of supposed ape men. Christian scholarship was withering under this blast. At every turn, however, there were at least a minority of Bible-believers trying to answer these great challenges, some more soundly than others. Philip Henry Gosse (1810–1888) believed in a young Earth, but attempted to make a distinction between what he called “diachronic” and “prochronic” time.<sup>7</sup> The fact that there was no real way to discriminate between these in his theory lead some (like VanDoodewaard) to believe he was teaching that God had created fossils in place. William Cockburn (1773–1858) had a more rigorous, scientific approach, but his views did not win the day. The author does not delve deeply into the solid defence made by the ‘scriptural geologists’ at this point in history,<sup>8</sup> perhaps leaving the reader with the impression that barely any defence was made.

### Compromise creeps in

In light of the growing opposition to biblical orthodoxy, it is not surprising that many Bible scholars experimented with their theology. Charles Hodge (1797–1878), while arguing for both gap and day-age theory at Princeton,

said the relationship between fact and revelation was an open question and that if we were to take Genesis in its ordinary sense: “[I]f that sense brings the Mosaic account into conflict with the facts, and another sense avoids such conflict, then it is obligatory for us to adopt that other.” He also argued for the fixity of species, even though he acknowledged that other Christians held to the belief of variation within a kind.

Spurgeon, the most famous preacher of the 19<sup>th</sup> century, also moved toward gap and day-age theories, although he never left a belief in a literal Adam and Eve. B.B. Warfield (1851–1921), however, would seem more like a theistic evolutionist, allowing for the possibility of an evolutionary origin of Adam and Eve, as long as it was guided by “divine providence”. Yet his good friend and colleague on the faculty of Princeton Theological Seminary, Geerhardus Vos (1862–1949), adeptly defended the literal interpretation. James Petigru Boyce, president of Southern Baptist Theological Seminary, had no truckle with long ages or evolution or pre-Adamites *in general*, as long as Adam and Eve were special creations.<sup>9</sup> Yet, as in the case of Vos, there were others arguing strenuously against these changes in direction, leading to many denominational splits.

Into this milieu comes William Jennings Bryan. He is not discussed in the book, but thinking about the theological context in which the 1925 Scopes trial occurred, and several things he said, especially while on the stand, brings certain events into clarity. For example, when pressed by Clarence Darrow with the old “Where did Cain get his wife?” question,<sup>10</sup> he did not reply coherently. Why? Because he, like many Christians of the day, had no problem with an old Earth or evolution. Adam and Eve, however, or at least their *souls*, had to be divinely created.<sup>11</sup> There was a wide theological gap here, and he knew it.

For example, perhaps Cain married a soulless hominid?

### Modern times

The latter portion of the book gets more into the history of specific denominations and denominational seminaries, some of whom more or less defended the literal hermeneutic, and some of which did the opposite. This will be interesting for the student of 20<sup>th</sup> Century theological history.

Seeing names like Davis Young, Meredith Kline, Bruce Waltke, Peter Enns, or Tim Keller talking about things like “levels of knowledge”, “accommodation”, “metaphor”, “literary”, “local flood”, or “primate ancestors” takes on a new meaning when one understands that these very same arguments are not at all new. Also, knowing that each of these had or has a conservative foil, even if that scholar was not as well known, is encouraging. The fact that modern theologians cannot evade the scholarship of past centuries means that no one has the right to simply accept a position without carefully analyzing the known ramifications. According to VanDoodewaard, the historical record, “... reveals a repeated pattern toward an erosion of scriptural inerrancy, sufficiency, and historic Christian theology.” While earlier alternative theologies included a real Adam and Eve, irrespective of what may have come before, more modern ones often do not.

In the final chapter the author outlines three different models of theistic evolution, including human evolution: 1) with divine impartation of the soul, 2) with only a divine relationship, or 3) with only divine revelation. He then describes at length the ramifications of these views on 10 subjects, including ethics and human life, marriage, the unity of race, human language, God as Creator, the goodness of creation, the effects of Adam’s fall, Christ as Creator and Redeemer, biblical covenants, and moral accountability. This

Pandora's box of non-literal theologies, with little internal scriptural coherence, tends to minimize the nature of death as a divine judgment—and the corollary that Jesus' death could atone for our sin. They “remove most, if not all, of the supernatural, temporally immediate aspects of creation” and, he concludes: “the end result is the complete loss of the gospel of our Lord Jesus Christ.”

This book is recommended reading.

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## Another evolution pillar demolished

*The Evolution Revolution—Why Thinking People are Rethinking the Theory of Evolution*

Lee Spetner

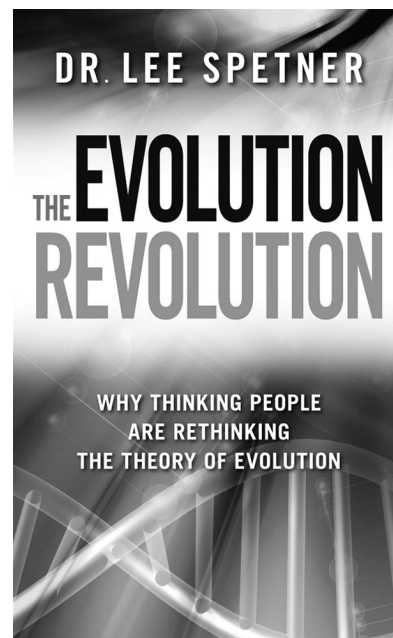
Judaica Press, Brooklyn, NY, 2014

Jerry Bergman

Most examples of evolution used by its supporters today to document their theory are termed ‘microevolution’ by some evolutionists. Creationists call this ‘variation within the Genesis kinds’. Evolutionists argue that macroevolution from one genus to another is simply large-scale microevolution, which, when allowed to operate for long periods of time, will produce macroevolution or major changes in all life forms. Spetner documents why many cases of this so-called microevolution evidence does not support common-ancestry evolution from single cells to humans by mutations and natural selection.

### Spetner's conversion

A common stereotype is that most people who reject Darwinism are uneducated Christians who rejected evolution due to their religion. Spetner is one of many persons that contradict this theory. Spetner, a Jew with a doctorate from MIT in science, rejected Darwinism due to his intensive and extensive research on the subject. He writes that his journey, which ended in rejecting Darwinism, began at a lecture by leading American geneticist and anti-eugenicist (Hiram) Bentley Glass (1906–2005) at Johns Hopkins University (figure 1), where Spetner was then teaching information theory.



This lecture caused Spetner to wonder about the source of the enormous amount of biological information existing in DNA in all life forms. For this reason he posed a question about the source of genetic information to Professor Glass. Glass responded that he never really thought about this problem (p. 7). Thus began Spetner's intellectual journey, researching the dilemma of new information coming into existence as life progressed. He ended up publishing a few papers on the topic in peer reviewed scientific journals, including *Nature* and *The Journal of Theoretical Biology*. In his research, after reading Dawkin's book *The Blind Watchmaker*, Spetner concluded that the standard explanation for Darwinism, according to its leading advocates,

“... didn't make sense. Random errors in copying the DNA and natural selection were supposed to account for the evolution of all life from some simple primitive cell. I

could not understand how random mutations and natural selection could account for the information buildup in what is called Common Descent. Could those DNA copying errors really bring new information into living organisms?” (p. 7).

His study led him to write his first book, *Not By Chance!*, published in Israel, then later in the United States. The common view of Darwinists was that the “vast amount of information contained in trees, fish, elephants, and people” came from “random mutations and natural selection.” Spetner concluded that this view was scientifically bankrupt. The problem was the fact that:

“Natural selection is supposed to be the magic that makes evolution happen, but all natural selection does is eliminate the less adaptive organisms and allow the more adaptive ones to survive and proliferate. Where do those more adaptive ones come from? Apparently, that’s what random mutations are supposed to accomplish” (p. 8).

This book examines in detail one solution to part of this problem—the theory that much adaptation is a result of complex inbuilt systems that respond to the environment, and not random mutations that are selected by natural selection.

A major section of the book documents Professor Spetner’s theory that much of the ‘microevolution’ observed in nature is a result of complex inbuilt mechanisms, such as epigenetics, that are influenced by the environment to inactivate certain genes and activate others. Many examples of this process are well known in bacteria. If certain types of sugar are present in the environment, and the preferred sugar type is lacking, the bacteria is stimulated to produce the enzymes necessary to utilize less preferred sugar types. If the preferred type of sugar is present, the bacterium does not need to waste energy and resources to produce the enzymes required to digest the other sugar type. Thus, the



Figure 1. Johns Hopkins University where Lee Spetner was professor.

environment affects bacterial gene expression by inactivating these genes.

A key evidence for the conclusion that microevolution cannot account for the changes that have been observed to occur in many life forms includes the fact that they occur with a speed that is far greater than can be accounted for by the “Neo-Darwinian mechanism of random mutations and natural selection” (p. 65).

Another problem is that supporters of Neo-Darwinian theory have always been vague about how the long strings of mutations that their theory requires can happen at just the proper time to allow each mutation in the sequence to have selective value over the previous non-mutation state (p. 66).

### Phenotypic-plasticity theory

Many other examples exist of what is now called the phenotypic-plasticity theory. A well-documented example is the pupfish that evolved very rapidly in response to environmental changes that occurred when they were moved from their original home into Devil’s Hole in Death Valley, the hottest and driest location in North America (p. 64).

After the pupfish were relocated, their inbuilt ability to adapt to this environment involved alterations of both their body shape and their behaviour to allow them to adapt

rapidly to Devil’s Hole’s very high average temperature and meager food resources. Their adaptation to this harsh environment required only a few years, which was far too rapidly for the necessary set of random mutations to achieve this task (p. 65).

To evaluate the phenotypic-plasticity theory, Spetner reviewed in some detail Sean Lema and his team’s pupfish research. They took newly hatched pupfish from the Amargosa River and reared them in the adverse conditions typical of Devil’s Hole. The biological effects of this major environmental change included alterations in their thyroid secretion levels. The behaviour changes that occurred were attributed to arginine vasotocin hormone changes and other adaptations.

The researchers also found several DNA regulation differences between the pupfish that were moved from the Devil’s Hole to the experimental refuge environment. Their findings supported the phenotypic-plasticity theory, and could not be explained by the mutation/natural selection evolutionary process (p. 65).

In another example, after David Reznick moved 200 guppies from Aripo to a tributary, changes occurred in only two years in the newly hatched guppy population, which was “much too short for random mutations and natural selection to have an effect”



(p. 72). Again, no new information was produced in the guppy's DNA, but an altered expression of existing information occurred. Spetner documents that even the famous well-documented evolution of Darwin's finches is also an example of this process. He writes that, in just 17 years or less,

"... the finches had diversified into various niches. If this diversification occurred in less than seventeen years, why did Darwin's Galapagos finches [as claimed by evolutionists] have to take two million years? They could have done it much more rapidly, and perhaps they indeed did. The diversification can be accounted for by a built-in response of the finch's genome to an environmental input" (p. 76).

Spetner gives many other examples of rapid evolution that are far better explained by inbuilt variation or regulation systems than by mutations and natural selection.

Spetner concluded by opining that biologists need to

"... stop pretending evolutionary events occur through random mutations and find out how they really occur. Biology has had an exciting ride in the twentieth century. Biology in the twenty-first century portends to be even more exciting" (p. 145).

His review of the literature has documented that, in many cases of so-called microevolution, adaptation was due to innate mechanisms that were designed to adapt to the local environment conditions, not mutations and natural selection as postulated by Darwinism.

His observations are shared by others, such as Professor Reznick, an evolutionary biologist at University of California at Riverside, who found that "some species are evolving far more quickly than Darwin ever imagined".<sup>1</sup> Specifically,

"Darwin had assumed that evolution takes tens to hundreds of thousands of generations to produce new species—a plodding path so slow it is essentially invisible. That theory still

held sway when Reznick began grad school in 1974. Scientists had studied evolution in controlled laboratory experiments, but watching it happen in a natural setting in a human lifetime was considered improbable at best, more likely impossible. ... Reznick says, 'People ... doubted I would live long enough to see the results'."<sup>1</sup>

It turned out that he did see clear evidence of rapid changes in 1981 when he

"... returned to Trinidad's swift streams to test his theory. He transplanted guppies from a site where they had to fend off cichlids, an aggressive, wide-mouthed fish, to a new site with no predators and no other guppies. Reznick also introduced cichlids to guppy sites without predators. He found that within four years—a mere six to eight generations—male guppies had significantly changed their reproductive patterns. Those transplanted from a high-predation site to a stream without predators were larger, matured later and reproduced more slowly. Where Reznick had introduced predators, the guppies adapted by maturing at an earlier age. Survival became a race to produce more babies."<sup>1</sup>

Other examples of rapid changes that random errors in DNA cannot achieve include the apple maggot fly (p. 70), guppies (p. 71), lizards (p. 72), and *Flavobacterium* (p. 56).

### Rapid evolution compounds the production of genetic trees

Spetner also tackled the phylogenetic tree challenge produced by Darwinists, showing that the tree produced depends heavily on the specific traits selected to produce the tree (p. 87). Select one set of traits and you will get one tree. Select another set of traits and you could produce another very different tree. And because phenotypic-plasticity theory can

explain some trait variation, it causes problems for constructing phenotypic trees. As millions of potential traits exist that could be compared, theoretically millions of different trees could be produced, some of which will be misleading due to phenotypic-plasticity events (pp. 88–89).

Related to phylogenetic trees are the many problems that exist in evolutionary convergence explanations for similar traits in very different life forms. This is a concept that has been illustrated with many examples, both by Spetner and others. A good example is the auditory system of mammals and that of certain insects, such as the South American rainforest katydid, which has a hearing system analogous to that of the vertebrates (p. 89).<sup>2</sup>

The theory postulates that life forms which are placed on very different parts of the phylogenetic tree and that do not have a recent common ancestor, must have independently evolved remarkably similar organs or structures. In this case, very similar hearing systems in life forms that were located on drastically different parts of the evolutionary tree.

Spetner noted that the authors of the katydid study called this "a notable case of convergence" which found that mammals and katydids "have evolved to hear in a markedly analogous way". Spetner then shows that the theory of convergence itself is problematic for many reasons, one of which is that genetic plasticity may account for some examples of convergence (p. 90).

In summary, this book is a *tour de force* of documentation that represents a major step in documenting the fact that the microevolution to macroevolution theory is problematic at its foundation.

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# No straight answers on animal death before the Fall

## ***Death Before the Fall: Biblical Literalism and the Problem of Animal Suffering***

Ronald E. Osborn

IVP Academic, Downers Grove, IL, 2014

Lita Cosner

For biblical creationists, a key argument against adding a billions-of-years timescale to Scripture has always been the problem of animal death and suffering preceding sin. If death is a consequence of sin—including animal death and human death—then how does the old-earth Christian explain the fossil record, which is a record of death they would place before any possible existence of Adam?

Because this is an issue many feel old-earth Christians do not address sufficiently, one might eagerly anticipate what Ronald Osborn has to say in *Death Before the Fall*. However, we aren't allowed to get far before he basically abandons any search for an answer to this admitted problem:

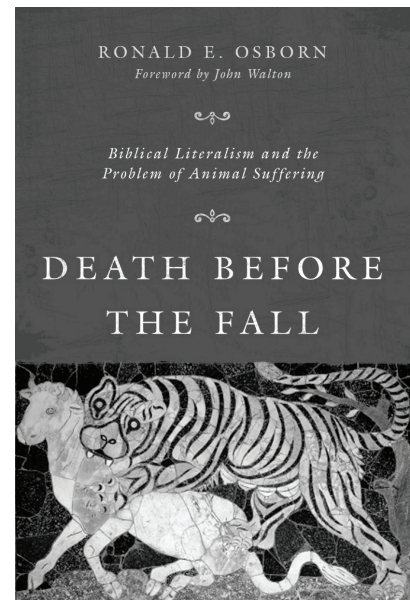
"Readers should be fairly warned from the outset that I offer few confident answers to the problem of animal suffering in the manner of some Christian apologists. Indeed, I usually find such 'answers' to be morally repellent in the face of the challenges, which I take to be insoluble this side of the parousia (and quite possibly the other side of the parousia as well). Nevertheless, it would be just as morally irresponsible to abandon the search for clues to the theodicy dilemma from a foregone conclusion that the search

can yield no answers. The ideas presented in these pages are offered in an open-ended, exploratory form based on the belief that partial answers do exist" (p. 20).

One of the most *disappointing* things about this book was the refusal to take any clear stand on the very issue that was the title of the book. But it can also be taken as a tacit admission that from the old-earth standpoint, no answer *exists* to this troubling question.

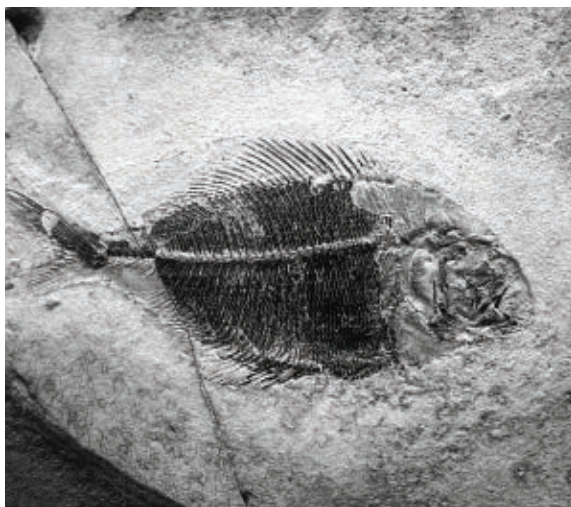
## **Discussing anything but the topic**

It takes Osborn a while to discuss anything regarding the issue of animal suffering and death before the Fall. First, he attacks the idea of biblical creation on several fronts. In Chapter 1, he argues that Scripture can be read to allow for progressive creation or theistic evolution. He says, "We are left entirely free to think that the Creator might be delighted to see his creation multiply not only in number but also in kind" (p. 26), and "God desires a world that will in some sense be free from his direct control, and the creation is in certain ways marked from the very first moment by the presence of freedom" (p. 27). There is no exegetical argument, particularly for the latter claim, and one is tempted to conclude that no serious exegesis with that conclusion is possible. Indeed, even the most cursory survey of the biblical texts about how God interacts with His creation seems to show that God is glorified by His complete knowledge and control over the animal kingdom. He feeds the birds (Matthew 6:26) and knows when even one falls to the ground (Matthew 10:29).



Osborn also claims that the God's appraisal of His creation as 'very good' (*tov me'od*) indicates that it was less than perfect, because the same term is used of Rebekah, meaning 'very beautiful', as well as of the Promised Land, both of which fell short of perfection. However, in the specific context of the creation narrative, we have the Creator's own appraisal of His work—which is different from the narrator's appraisal of Rebekah's beauty, not intending to say anything about *moral* perfection. And *tov me'od* culminates six other statements that God's creative work has been *tov*; it is clear that Scripture intends to present a perfect creation completely in line with God's will. If there was any death and suffering, it would have to have been death and suffering that God intentionally created and willed, which *would* create a very real theodicy problem.

In Chapter 2, Osborn argues that biblical creation is a relatively new phenomenon. It's true that the specialized area of *apologetics* devoted to defending the biblical doctrine of creation and bringing the relevant scientific facts to bear on the topic is a fairly recent development. However, there is a long line of biblical interpreters, theologians, and scientists



**Figure 1.** Old-earth creationists had no good explanation for the death and suffering of creatures that they say lived long before Adam was created.

who have believed and defended the biblical doctrine of creation. Indeed, it could be argued that creation apologetics is the logical outgrowth of the same sort of belief in biblical creation in a context where the doctrine is being specifically attacked and undermined in the church. The lack of a specialized area of creation apologetics in the early church should therefore be taken as evidence of the universality of belief in creation—it simply wasn't even debated.

In Chapter 3, Osborn criticizes CMI in particular for using the James Barr quote, which claims that he (Barr) knew of no professor of Hebrew or Old Testament at any world-class university who did not believe Genesis intended to portray a 6-day creation. First, Osborn claims that we do not cite it correctly and it is hard to find. In fact, CMI has provided more information to anyone who has ever asked for it,<sup>1</sup> and we received a copy from the original recipient of the letter with permission to reuse it. But, furthermore, Osborn claims that Barr was wrong, and cites Walter Brueggemann as a scholar of whom Barr should have been aware. There is no indication he wasn't—though Brueggemann was not, and has not since been, a professor at a 'world-class university'.

Barr's statement only covered a narrow, elite group of scholars, and no-one has been able to bring up a counter-example to prove Barr wrong.

Osborn also brings up tired arguments about Adam having been created before plants according to Genesis 2 and that the events of Day 6 requiring a long period of time. He certainly was able to cite CMI to criticize the use of

Barr's letter; he might have done some further research in creation literature to find that we have already exhaustively addressed these arguments. What he does not bring up is that the Apostle Paul believed the Genesis account of Day 6, as shown when he said, "Adam was formed first, then Eve" (1 Timothy 2:13).

In Chapter 4, Osborn argues that creation is bad science, because it will not admit evidence against the paradigm. But that could be said about evolution just as easily. The problem with this criticism is that when we are dealing with historical science, what we believe happened in the past plays a large role in how we interpret the evidence. In Chapter 5, Osborn invokes Newton and Boyle as scientists who championed methodological naturalism. Most creation scientists would agree that when it comes to operational science, methodological naturalism is appropriate (answering "God made it that way", while true, is not a *sufficient* answer when we are dealing with operational science—that does not mean that there are not questions of *historical* science which demand supernatural answers).

In Chapter 6, Osborn comes very close to claiming that creationists take

the Bible literally because they are psychologically disturbed. He gives some psychological indicators, then summarizes, "We can now see that fundamentalism, in its often uncompromising literalistic stance toward Genesis, has as much to do with the peculiar psychological makeup of individuals as it does with abstract theological reasoning" (p. 82). It takes breathtaking chutzpah to associate an entire movement with psychological problems, though it does take a bit of the burden off one to prove one's point if you can claim the other person is mentally unstable.

But then, in Chapter 7, Osborn takes it a step further and associates biblical creation with Gnosticism: "In their zeal to define others out of the life of the Christian faith ..., fundamentalist creationists themselves can quickly come to exhibit all the marks of a very ancient heresy" (p. 86). One might notice that, in his zeal to discredit creationists, he has argued himself into a veritable bear trap of an argument. Ancient Gnostics believed that the Demiurge, an evil lower god, created the world, and physical matter was inherently bad. Spirit was seen to be inherently good, and the goal of the Gnostics was to escape the physical world. Creationists believe that God created the world good—therefore physical matter was originally 'very good'. This has been marred *but not obliterated* by the Fall—God Himself became incarnate as an actual human—and God's plan is to *restore* the created world, not simply destroy it. The future new heavens and earth Christians look forward to is a *physical* restored creation. There is simply nothing Gnosticism and biblical creationists have in common, and Osborn loses even more credibility with this argument.

In Chapter 8, Osborn argues that certain theologians interpreted Genesis figuratively. He gives four examples: Barth, Calvin, Augustine, and



Maimonides. Barth was a modern neo-Orthodox theologian who denied biblical inerrancy, and we should feel very free to say he was wrong. Calvin and Augustine were biblical creationists, as shown in *Refuting Compromise*.<sup>2</sup> And Maimonides was a medieval Jew who was influenced more by antibiblical Jewish tradition (e.g. the Muslim Avicenna and the Greek Aristotle) than by the Scriptures themselves; why would a Bible-believing Christian go to a Jew who rejected Christ to learn about the Scriptures, which we believe pointed to Him?

In Chapter 9, Osborn criticizes those who expect professors at Christian colleges to teach according to a statement of faith that includes creation. He advocates allowing for ‘loyal dissent’ regarding theistic evolution and old-earth views. However, open theists

and Unitarians could also claim ‘loyal dissent’—who decides what the difference is between heterodoxy and ‘loyal dissent’? CMI has always acknowledged differences between Christians that result from different readings of Scripture—like Calvinism vs Arminianism, for example, where both sides hold Scripture to be inerrant and authoritative, but *interpret* it differently—and differences that result from different *authorities*. For instance, it is impossible to interpret Scripture itself as speaking about billions of years; one has to import that idea from modern science. This, in effect, makes science the *authority* over Scripture. This is standard creationist argument, and it would have been nice to see Osborn interact with it, or even acknowledge it.<sup>3</sup> It is one thing to appeal to different

philosophical views and advocate for an openness where all sorts of differences are accepted as ‘loyal dissent’, but quite another when someone is ‘dissenting’ against Scripture’s clear testimony; that has never been accepted as a good thing by Christians.

There are 14 chapters in Osborn’s book, and 179 pages of text, not counting the endnotes. So it is significant that we arrive at Chapter 10 and page 126 before Osborn gets around to actually discussing what was supposed to be the subject of his book. He claims that evolution actually solves the theodicy problem of animal suffering “albeit through

the elimination of the Subject who makes the problem a moral problem as such” (p. 126). He argues:

“We must confront the magnitude of animal suffering and death occurring every instant of every day, which evolutionary theory did not create but which it at least has the theological advantage of explaining in a way that does not directly attribute the harshest facts of nature to God’s wrathful response to human sin” (p. 127).

“It is time that biblical literalists at least candidly acknowledge that the challenges they face are not only scientific but theological and moral as well, and that these problems are no less great for them than for process creationists or theistic evolutionists” (p. 128).

The response of the biblical creationist is simple: God created the world, so He has the right to demand obedience of His creatures. When Adam rebelled against God, His response showed the utterly serious and disastrous nature of sin—the whole world was thrown into chaos. It is not our place to tell God that His punishment was too severe or that animals did not deserve to be punished for humans’ sin. In fact, if we view Adam as the federal head of creation, it is logical that not only he and his descendants, but everything under his dominion, would suffer as a result of his sin.

Osborn also claims that, because without death eventually the world would become filled and there would be no more birth, such a world would not really be ‘very good’ (p. 129). Certainly, “be fruitful and multiply” was God’s very good design to fill His creation. But Scripture also looks forward to a time when men and women no longer marry or are given in marriage (Matthew 22:30). So the new heavens and earth—which is the culmination of God’s salvific plan—would not be ‘very good’ by Osborn’s definition!



Figure 2. Osborn’s interpretation of *tov me’od* in the creation account does not take into account its context.

### Does young-earth creation require God to deceive?

Osborn claims that biblical creationists are forced to believe in a God who deceives, because He created differently than science seems to indicate:

“Most young earth or young life creationists I have spoken with, when pressed about the weight of empirical evidence, concede that their models cannot explain the physical data from biology and geology in any kind of satisfying way, and that they would have never have arrived at their views were it not for the fact that they begin with a very particular set of assumptions about how the biblical text must be read” (p. 131).

Unfortunately, he does not cite a specific creationist or give a direct quote. But creationists have *always* maintained that what we see in biology and geology *today* cannot fully explain the *origin* of these things. Rather, we appeal to supernatural creation to explain the origin of life and its complexity, and we appeal to the supernatural judgment of Noah’s Flood to explain much of the geological record. Because evolutionists must also appeal to things that defy the laws of physics as we understand them, they are also appealing to ‘miraculous’ origins, albeit without a miracle-worker.

This does not make God a deceiver, however, because He *told* us plainly in Scripture how He created. In fact, deception or truth can only be communicated in *language* and propositional statements. (Tree rings and geological layers do not communicate anything *as such* but must be interpreted.) Rather, if God had created over billions of years, He would be a deceiver, because He communicated in Scripture that it happened quite differently.

In Chapter 11, Osborn offers a ‘midrash’ wherein Adam’s role was to restore an already-corrupted creation but took Satan’s side rather than God’s.

So Christ, whom Osborn wrongly calls the ‘second’, rather than ‘last’, Adam, did what Adam failed to (and could not) do. However, in this (Osborn’s) scheme, Adam did not introduce death through his sin—he only failed to *defeat* death, which would have already existed. This is sub-biblical and therefore unacceptable to the person who takes Paul’s theology seriously. In Chapter 12, Osborn admits that he has reservations with some of the weaknesses in this line of reasoning, and, like Hugh Ross,<sup>4</sup> points to Job, where God is glorified by providing food for lions and other carnivorous creatures. But this only shows that God is glorified by how He operates in the fallen universe, not that He set things up this way in the first place. Rather, Isaiah 11 and 65 point to the eschatological future where lions will eat straw—i.e., God will still provide their food, but it will no longer be other animals! Given that in Genesis plants are said to have been food for both plants and animals before the Fall (Genesis 1:29–30), it makes much more sense to see Eden and the eschatological order as reflective of God’s true estimation of what is ‘very good’. Indeed, commentators on Isaiah agree that he made Edenic allusions in those chapters.<sup>5,6</sup>

In Chapter 13, Osborn takes on the biblical creationist argument that a literal reading of the creation account is required in order to make sense of the Atonement. Osborn responds that the way we view the atonement is wrong: “... strictly penal-substitutionary readings of Christ’s death and resurrection rest upon a relatively late and individualistic turn in Christian thinking” (p. 160). Rather, Osborn argues “God creates as he redeems and redeems as he creates so that the two are always part of the same act” (p. 160). But what did the *to’v me’od* creation need redemption from? And what does it imply about salvation if Christ’s salvific work

represents not the answer to Adam’s sin and that of his descendants, but the solution to a problem God Himself wove into creation from the start? Most Christians would be disturbed by this theory, but it is actually startlingly honest of Osborn to practically admit his view is incompatible with Substitutionary Atonement.

### Conclusion

A book should be judged by its own standards. What does it set out to accomplish? What does it promise the reader? With the title, Ronald Osborn promised a discussion and at least a proposed answer to the problem of animal suffering. He spent well over half the book talking about things only tangentially related to his topic, and then when he got to the topic, he still found countless ways to rabbit-trail away from the matter at hand. Ronald Osborn failed at what he set out to do, and didn’t really accomplish anything else in its stead. *Death Before the Fall* could have been an interesting and challenging book, but unfortunately it simply showed that when it comes to death and suffering before the Fall, neither old-earth creation nor theistic evolution have satisfying answers.

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# John Walton reimagines Adam and Eve

*The Lost World of Adam and Eve*

John H. Walton

InterVarsity Press, Downers Grove, IL, 2015

Keaton Halley

In this third book of his ‘Lost World’ series, John Walton, professor of Old Testament at Wheaton College and Graduate School, weighs in on the current debate over the historical Adam. Since he admits that he’s bought into what he deems the “scientific consensus” on evolution (p. 204), it is quite convenient that he reaches this conclusion: the Bible makes “no claims” about “biological human origins” (p. 181). That is, the Bible does not say when, where, or how people began, except that God was involved.

Walton at least believes that Adam and Eve were a historical couple. But, he says, they were not necessarily “the first human beings, the only human beings or the universal ancestors of all human beings” (p. 103). In 2009, Walton held that there was both “material and spiritual discontinuity” between Adam and “prehuman hominids”.<sup>1</sup> But now he is comfortable with the idea that Adam was “born of a woman” (p. 76) and that, as N.T. Wright says in his contribution to chapter 19, “perhaps ... *God chose one pair from the rest of the early hominids*” (p. 177). However, Walton is severely misreading the Scriptures, erecting his case on a foundation of errors in judgment, logic, and exegesis. This review will explore just a handful of Walton’s missteps.

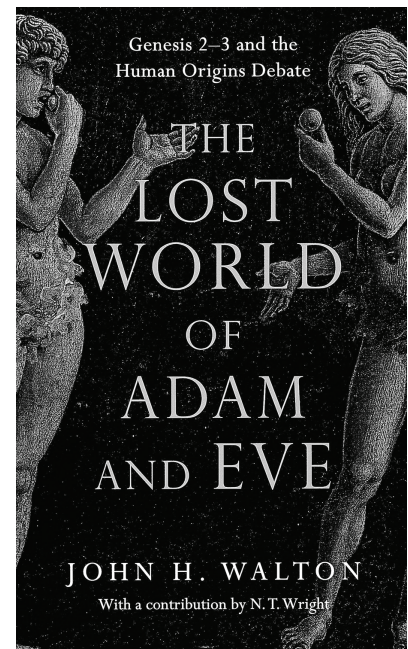
## Subverting inerrancy

While claiming to believe in biblical inerrancy, Walton denies it in practice. He engages in doublespeak—saying, on the one hand, “Inerrancy pertains to that which the text affirms” but, in the preceding paragraph, claiming that “the text affirms” a falsehood—that people literally think with their hearts—an idea which he “can safely set aside” (p. 201). In biblical imagery, however, the ‘heart’ was an idiom for the mind, just as today it’s an idiom for love—no one thinks that the blood pump literally ‘loves’.

Walton also supposes that the Bible preserves the following wrong beliefs of its human authors: intestines are likewise used for thinking (p. 18), the sky is solid (pp. 18–20), and the sun and moon are very nearby (p. 39). Again, Walton is speaking out of both sides of his mouth when he says that the “text does not affirm” these beliefs (pp. 20–21). He is correct there. But then how can he supposedly determine from the text that the authors believed such falsehoods, as opposed to using idioms of their day?

At least Walton discloses his method for distinguishing between biblical affirmations we are free to reject and those which are authoritative and binding. It depends on “whether the text hangs theology on the belief” (p. 201). However, the doctrine of inerrancy itself is theological—what Scripture says, God says (2 Timothy 3:16). Therefore, Walton’s criterion should not allow him to reject any biblical affirmations since theology is always on the line, no matter how incidental the subject.

Nevertheless, Walton justifies his selective denial of biblical claims by



appealing to the notion that, as God inspired Scripture, He was “accommodating ... current thinking” (p. 201). This in itself is hard to understand, since God so often *corrected* ‘current thinking’ if it was wrong, as Jesus, God Incarnate, did in the Gospels. But when Walton cites John Calvin to legitimize his concept of accommodation (p. 202), it is clear that he conflates *simplifying* the message with *embracing error*—only the first of which is consistent with inerrancy.

## Redefining creation

Because this book builds upon his earlier work, Walton revisits his outlandish claim that Genesis 1 is exclusively about *functional* origins, making absolutely no reference to *material* origins. This has many problems, not the least of which is that the rest of the Bible takes Genesis 1 to refer to material creation.<sup>2</sup> Moreover, if Walton is wrong about the Bible’s teaching on origins in general, his specific claims about human origins crumble.



### Adam as archetype

For Walton to maintain his thesis that Genesis is silent about the material origin of humanity, he must explain away the accounts of God forming Adam and Eve. Thus, his “core proposal” is that those accounts “should be understood archetypally”—meaning they speak not just about individuals but about a larger group to which the individuals belong (p. 74).

Regarding Adam, then, Walton claims that there is nothing unique about the fact that he was formed from dust. The Bible says that people in general were made from dust and return to dust (Job 10:8–9; 34:15; Psalm 90:3; 103:14; 104:29; Ecclesiastes 3:20; 12:7) so Walton believes this merely alludes to human mortality. In this sense, he asserts, Adam could be ‘made from dust’ (i.e. mortal) and still be the offspring of earlier human ancestors.

As for Eve, Walton says she was not the result of surgery performed on Adam’s ribcage, even though that’s what the text indicates. Rather, as Adam went into “a deep sleep” (Genesis 2:21), he dreamt about being divided in two, with one of his halves becoming Eve. According to Walton, the archetypal truth this conveys is that “All womankind is ‘from the side’ of all mankind” (p. 80).

While there is some merit to Walton’s claims about archetypes, the problem is that he regularly sets up the archetypal and individual interpretations as though one must choose between them. For example: “Once the forming accounts are recognized as archetypal, they cease to be meaningful in terms of chronology or history of material human origins” (p. 200). This is a false dichotomy. While Walton recognizes that Adam himself is both historical and archetypal, he doesn’t consider that ‘being made from dust’ can be both as well. But biblical archetypes often work this way. All believers “have been crucified with

Christ” (Galatians 2:20), yet this is only figuratively true of us because it was literally and historically true of Jesus. Plus, we were literally made from dust in a *collective* sense due to the fact that we all go back to Adam.

Furthermore, there is textual evidence that Adam was formed from dust in a unique, historical sense. For one thing, the references to others’ formation from or return to dust occur in poetic passages, while Adam’s formation in Genesis 2:7 is historical narrative. Also, taking v. 7 as a nod to Adam’s mortality may be anachronistic, since it’s not until 3:19 that God spoke of reversing the process and sending Adam back to dust.

Besides, Walton’s interpretation makes no sense of the context in which Genesis 2:7 occurs. Verse 5 describes the setting, highlighting the lack of a “man to work the ground.” So, v. 7 should be seen as the provision of what was lacking. But highlighting human mortality is no solution to the absence of man; *creating* man is.

Also, there is textual evidence that Eve was built from a rib in a unique, historical sense. Again, the account is historical narrative and the context is about supplying a helper fit for Adam. But if the text doesn’t describe Eve’s material origin and only points to the universal truth that women are natural counterparts to men, then we have no idea where Eve came from. She along with other women might have been around before this time. If so, then why could Adam not find a suitable helper and why would he be in a position to name the entire gender—saying, “she shall be called Woman”—if females were already a category familiar to him and they preceded him?

Furthermore, the idea that this takes place in a vision is fanciful. Genesis 2:21 mentions God closing up the location where He had removed part of Adam but this detail is only worth stating if God actually performed surgery, so readers know that

Adam was repaired. Plus, using ‘flesh’ to ‘close’ the ‘place’ makes perfect sense if this was a small incision but is strongly incongruent with Adam being split in two since, in that case, Adam wouldn’t need patching up—he would need half of his body to grow back!

In addition, the New Testament authors treat the formation narratives as unique historical events. In 1 Timothy 2:13, for example, Paul makes a theological point about the roles of men and women based on the chronology of their origins. He says, “Adam was formed first, then Eve.” But this would be incoherent if Paul understood Adam’s ‘formation’ as a declaration of mortality rather than Adam’s individual coming into existence. Walton even admits that Paul is not using Adam and Eve archetypally in this verse (p. 95) but fails to recognize how this contradicts his interpretation of Genesis.

Similarly, in 1 Corinthians 11:8–12 (a passage Walton does not address), Paul says that just “as woman was made from man, so man is now born from woman.” Paul distinguishes between what happened in the past and what happens today, yet treats both as historical events, indicating that Eve’s formation did not happen in some symbolic dream world but in reality.

### Decoupling Genesis 1 and 2

Because most Christians understand that both Genesis 1 and 2 describe the origin of humans, it makes sense to read chapter 2 as an elaboration of the events of Day 6. Walton instead sees Genesis 2 as a ‘sequel’ involving events that may have taken place long afterwards. Therefore, “the people in Genesis 1 may not be Adam and Eve, or at least not only Adam and Eve” (p. 64). The trouble is, this can’t be sustained biblically.

On the one hand, Walton’s attempts to drive a wedge between Genesis 1 and 2 are weak. For example, Walton



raises the old canard about contrary sequences of events. He claims that plants came before man in Genesis 1 but after man according to Genesis 2:5–6. Only two pages later, however, Walton has forgotten his own challenge, now recognizing that Genesis 2:5–6 describes “cultivated crops rather than the general vegetation of Genesis 1” (p. 66). So there is no contradiction here. Well, not in the Bible—just in Walton’s argument.

Likewise, Walton claims that animals came before man in Genesis 1 but vice versa in Genesis 2. But, again, the animals in chapter 2 could be a subset of the groups previously created or, as many translators and commentators have recognized, the verb in v. 19 may faithfully be rendered as “had formed”.

Walton’s other arguments about there being too much activity in Genesis 2 for 24 hours and Cain’s encounters with alleged non-relatives have been answered long ago.<sup>3</sup> Also, Walton’s argument about the word *toledot* (translated: “generations” or “account”) in Genesis 2:4—supposedly serving as a clear indicator that events in that section occur after the previous section—is undermined by his own admission that there are chronological overlaps in several other adjacent *toledot* sections (p. 65).

In fact, there are NT texts which tie Genesis 1 and 2 close together in time but Walton fails to interact with them. In Matthew 19, for example, Jesus connects the “one flesh” couple in Genesis 2 with the “male and female” of Genesis 1 and says that God established marriage “from the beginning” (Matthew 19:4, 8), not generations down the road. Many other NT passages similarly place events closely associated with Adam and Eve at the foundation of the world, ruling out Walton’s long time gap between Genesis 1 and 2.<sup>4,5</sup>

Also, 1 Corinthians 15:49 says that all people bear Adam’s image and, in



Figures 1. The creation of Adam and Eve in Paradise by Hinrich Luckander, 1759–1792.

context, this means (at least) having the same kind of weak and perishable body that he had, in contrast with the imperishable bodies believers will one day receive, whereupon—according to the text—we will bear Christ’s image. But, especially given

Genesis 5:3 which says that Adam passed his image on to Seth, the fact that all bear the image of Adam is most naturally explained by our descent from him. We receive Christ’s image through supernatural transformation but, apart from this, Adam’s image



must have been transferred through inheritance—confirming Adam as father of all.

### Misconstruing motherhood

Although she is called “the mother of all living” (Genesis 3:20), Walton claims that this does not prove “all humans are genetically descended from Eve” (p. 187). He says such an expression is not indicative of biology, since Jabal and Jubal were the fathers “of those who dwell in tents and have livestock” and “who play the lyre and the pipe” (Genesis 4:20–21). But, as usual, Walton has ignored the differences in context. Jabal and Jubal started disciplines which they passed on to others and in this way played a fatherly role to those who followed in their footsteps. But how is Eve’s motherly role anything like that? Eve did not invent the discipline of ‘living’ and pass that on to non-relatives. There is no reason to think that she would be a mother to all in any sense unless she and Adam were the biological progenitors of the entire human race.

### Nations from Noah?

Regarding Paul’s proclamation that God “made from one man every nation of mankind” (Acts 17:26), Walton says he is referring to Noah, not Adam, and has a geopolitical focus, not a biological focus. However, the idea here is not that national entities were formed when existing people organized and established governments; it’s that all people groups trace their ancestry back to one person. As Walton admits, “The nations come into being through lines of descendants” (p. 186), so this absolutely does concern biology! And, given this, it is unlikely that Paul was referring to Noah. Paul’s language is very universal, speaking of God as the Creator of all things (v. 24) and the Sustainer of all mankind (v. 25). So Paul considered this “one” to be

the universal biological ancestor of all people. Noah did not give rise to the women on the Ark or the people living before the Flood—but Adam did.

### First in line

Walton notes “that the genealogies consistently go back to Adam” and Luke 3 goes one step further, “back to God” (p. 188) but he denies the implication that Adam was the first man. Walton argues that Luke presents “a lineage through Joseph, so it is specifically *not* his biological lineage” and he says Luke may have added the “connection to God” because it signified Adam’s federal headship or his priestly role (pp. 188–189).

However, the genealogies—including Luke’s—are about father/son relationships, so most of the links are biological, even if there are exceptions to the rule with links involving adoptions or in-laws. Also, as many have argued, Luke’s genealogy probably gives Mary’s lineage using Joseph’s name in place of hers (as son-in-law or adoptive son of Mary’s father Heli), since Jewish custom then traced ancestry through males.<sup>6,7</sup>

Plus, Luke does not merely claim that Adam was ‘connected’ to God; he indicates that Adam was the “[son] of God.”<sup>8</sup> Walton doesn’t give us any examples where that designation indicates federal headship or a priestly role, nor does he explain how this context supports those meanings. But the Bible certainly calls angels “sons of God” (Job 1:6; 2:1; 38:7; cf. Ps. 29:1; 89:6), likely because they had no forebears besides their Creator. And that meaning fits nicely into Luke 3.

### Sinful pre-Adamites

Walton also argues that death did not result from Adam’s sin but that Adam and Eve merely failed to secure the antidote to death. He doesn’t think the Bible precludes even

human death before the Fall (pp. 144–145, 159)—another area where his views have wandered further from Scripture over time.<sup>9</sup> In fact, Walton now believes there could have been “personal evil” before the Fall, which he defines as “antisocial behavior that causes suffering in others” (p. 154). He states, “anthropological evidence for violence in the earliest populations deemed human would indicate that there was never a time when sinful ... behavior was not present” (p. 154) but here his eisegesis results from treating evolutionary history as a given.

Walton tries to maintain a distinction between pre-Fall and post-Fall evildoers by abusing Romans 5:13 (“sin is not counted where there is no law”). On the basis of this verse, he claims that God didn’t hold anyone accountable for their actions until Adam and Eve disobeyed His command. However, in context, Romans 5:13 is speaking of the *Mosaic* law. This is why Paul says in v. 14 that “death reigned from Adam to Moses,” not prior to that. Paul’s point is that sin and its deadly consequences were present even for those without the law of Moses. When he says their sins were “not counted” he does not mean that these people weren’t being held accountable at all—only that the full scope of their violations was made more explicit later, after which they were *more* accountable. This is consistent with v. 20, which says, “the law came in to increase the trespass.” But nothing like this is ever said of Adam’s sin. Adam did not increase human sin; he introduced it. Paul explicitly says that “sin came into the world through one man, and death through sin” (Romans 5:12), “death reigned from Adam” (Romans 5:14), and “by man came death... For as in Adam all die” (1 Corinthians 15:21–22). Unfortunately, Walton doesn’t treat these passages with the seriousness they deserve.



### Adamant about Adam

Walton's exegesis of biblical texts is often creative and original—but that is not a good thing. Unfortunately, he is quite influential, judging by the adulation he receives in the book's blurbs. So creationists would do well to become familiar with Walton's thinking in general and this book in particular.

Despite Walton's monumental efforts to deny it, however, the Bible has much to say about human origins. Adam and Eve were not only historical but our first parents, supernaturally created just the way the Bible says.

Hopefully, this review will serve to expose Walton's egregious mishandling of Scripture and to prevent his brand of compromise from spreading further.

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# Darwin, Victorian England, Eugenics, and a new evolution

***Evolution Revolution: Evolution is True. Darwin is Wrong. This Changes Everything***

Alan Bennett

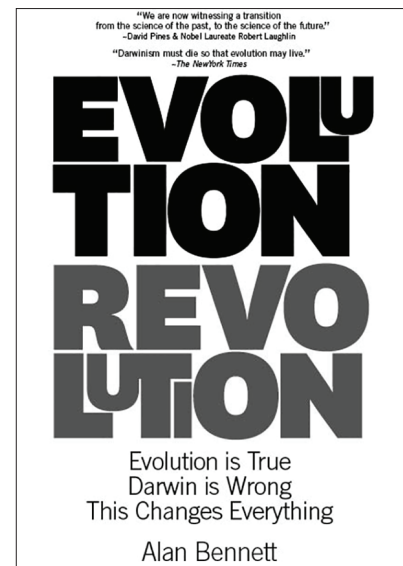
Lexem Publishing, 2014

John Woodmorappe

The author of *Evolution Revolution* is identified as a graduate of the prestigious Columbia University. He has been doing years of research at the Columbia Medical Center.

This work is eye-opening in a number of ways. It upends many popular myths about public resistance to the ideas of Charles Darwin. It challenges the notion that Darwin and his supporters were simply absorbing and repeating the racist ethos of their times. In actuality, eugenics was deeply interwoven within the very fabric of Darwinism. The elimination of unfit peoples was not some kind of collateral belief arising out of the social constructs of Victorian England. It was the very motive behind, and the very essence of, Darwin's *Origin of Species*.

The author proposes that current evolutionary theory relies too much on genetic changes, and he proposes an alternative theory of evolution. In it, evolutionary changes are driven primarily by alleged self-organizing principles, by the modification of regulatory networks that govern gene expression, and by sequential events in embryonic development.

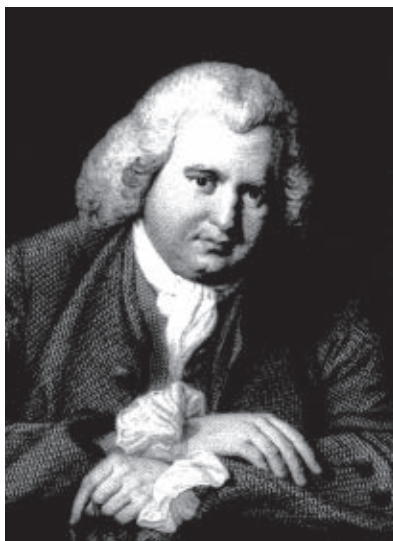


### Evolutionistic dominance long before Darwin

Evolutionary thinking goes back at least as far as ancient Greece, notably to the ideas of Anaximander (c. 610 – c. 564 BC). The author provides an impressive body of evidence for the many evolutionary thinkers that functioned for some 150 years before Darwin. They included Gottfried Leibniz, Pierre Louis Maupertuis, James Burnett, George-Louis Leclerc (Comte de Buffon), Marquis de Condorcet, Erasmus Darwin (figure 1), Etienne Geoffroy Saint-Hilaire, and Robert Grant.

However, Bennett goes beyond all this. He suggests that evolution was already widely accepted by the time of Darwin. In this respect, Bennett concurs with creationist authors, such as the late Henry M. Morris.

The widespread acceptance of organic evolution long before Darwin had implications for the belief in the



**Figure 1.** Erasmus Darwin, grandfather of Charles Darwin, and one of the many influential evolutionists that had predated Charles Darwin.

old earth and the geologic column. Many authors have argued that the old earth and geologic column were in no sense based on organic evolution, because, according to their argument, acceptance of organic evolution postdated them. Bennett's conclusion makes it obvious that, to the contrary, belief in organic evolution was already prevalent. This could not help but exert a subtle influence on the emergence of beliefs in the great antiquity of the earth and the existence of the geologic column.

### **Darwin merely replaced theistic evolution with atheistic evolution**

What exactly did Darwin do? According to popular misconception, the Victorian English generally believed in a literal 6-day creation. When Darwin wrote the *Origin of Species*, he met with a storm of religious hostility, and there was a brief "war between science and religion". Soon thereafter, educated people (including Christians) supposedly humbly bowed before the evidence, and abandoned their beliefs in the 6-day fiat creation in

favour of Darwin's brilliant insights. Bennett decisively rejects the foregoing scenario. He points out that Victorians already generally believed in evolution, and had done so well before Darwin, if only because it fit the "human progress" zeitgeist of the 19<sup>th</sup> century. However, the Victorians held to a "God was behind it" view of evolution, and *that* is what Darwin sought to eliminate.

A corollary misconception would have us believe that Darwin's ideas shocked Victorian England because they upset the cherished notion that humans are special, and did so in the rude manner of portraying humans as "descended from the apes". In contrast, Bennett shows that the evolutionary origin of humans, from non-human primates, was widely accepted long before Darwin. Several pre-Darwinian scientists, such as James Burnett and Jean Baptiste Lamarck, had written openly and freely about humans being descended from apes (p. 86). The oft-retold story of the ape-descent confrontation of Bishop Wilberforce and 'Darwin's bulldog' Thomas Huxley finds no support in the original sources (p. 92). It is probably a rationalistic fairy tale.

Bennett elaborates on how Darwin was out to replace theistic evolution with atheistic evolution:

"Neither natural selection and the idea evolution as a competitive struggle for existence, nor the idea that evolution is like a branching tree were original to Darwin. More importantly Darwin organized *The Origin* to argue against belief in 'special-creation' rather than other scientific explanations for evolution. His goal was to refute the belief that evolution was based on a 'Divine Design'. Darwin's target was not science, but society. What was later called 'Social Darwinism' was baked into his theory from the beginning" (pp. 65–66).

In other words, Darwin was not attempting to upend six-day fiat creation, as this was not much believed by Darwin's time. Instead, Darwin was attempting to upend what may be called theistic evolution, and to replace God-involved evolution with God-less evolution.

From a theological perspective, the foregoing developments once again illustrate the incremental rejection of God in Christian-dominated societies. This creeping atheism works as follows: first make God unbiblical and remote (the old earth and the geologic column), then make God into a vague behind-the-scenes tinkerer (theistic evolution), and then finally eliminate God altogether (as Darwin did).

### **The Industrial Revolution, capitalism, and eugenics**

Charles Darwin thought that what now is called social Darwinism was part of the very essence of biological Darwinism, and not (as commonly supposed today) some kind of add-on or misunderstanding of Darwinian evolution. Bennett considers Darwin an atheistic eugenicist and identifies the agenda behind his *Origin*:

"Darwin's goal was to arrange the evidence for evolution in a way that 'scientifically' justified eugenics as a solution to the social problems of the working class. He would use the same evidence to make the case that belief in evolution and God—science and religion—are irreconcilable. You can believe in one or the other, but not both. Society would have to choose: belief in evolution and science, or belief in God and religion" (p. 66).

To understand why Darwin thought this way, the reader must first appreciate the massive changes in English society in the century before Darwin.

### Darwinism: a remedy for Victorian social problems

Bennett mentions the poverty of the working classes, but rejects the common notion, derived from Marxism, that early capitalism was a black-and-white exploitation of working peoples. He comments:

“For a thousand years, England had been home to about four million people, mostly rural peasants led by a small group of aristocrats. In 1750, this abruptly changed. The Industrial Revolution transformed agriculture, forcing thousands of peasants off the land and into cities where they worked in factories and became a potent new social force—the ‘working class’. Wealth from the Industrial Revolution made possible safer water, better sanitation and vaccinations, all of which sharply reduced the death rate of working class children. The four million Britons of 1750 doubled to eight million by 1800, and reached a staggering 17 million by 1850” (p. 83).

So what does this have to do with Darwin? Everything. Darwin, and others who thought like him, were alarmed by the proliferation of the ‘lower orders’ in the wake of the Industrial Revolution. Worse yet, the inferiority of the ‘masses’ was innate and biological, and, contrary to the idealistic beliefs of many Christian activists, could not be corrected by such things as education and social reform. Something had to be done. Why not let ‘nature take its course’, so that the weak, inferior, and unfit would be allowed to die out? However, nature is too slow, and so humans must speed it up. Eugenics, including the mass sterilization of ‘undesirables’, would solve the problem. However, eugenic procedures would be objectionable to most people. For this reason, Victorian society had to be transformed so that it accepted eugenic procedures in the name of science and scientific progress.

If God could be removed from the picture, so much the better. That is why Darwin propounded his version of evolution, in which God plays no role, and in which the ruthless removal of the unfit is a natural and inevitable process.

### Eugenics and Darwinism

Throughout the first several decades after the publication of *The Origin of Species* (1859), eugenics dominated evolutionary thinking. It was a given. Bennett provides many examples of this, and comments:

“Held up as the ‘scientific’ solution to social problems, eugenics programs spread rapidly in the early 20<sup>th</sup> century, to France, Germany, the Soviet Union, and dozens of other countries. In the United States, tens of thousands had their children taken away and were sterilized, lobotomized ... and worse. The connection between Darwinism and eugenics cannot be dismissed as the abuse of Darwin’s ideas by others. Those who created modern Darwinism were the same people who created the modern eugenics movement. *The eugenicists were the Darwinists* [emphasis in original]” (p. 115).

Indeed, the leading eugenicists were Darwin’s own family members, as another author commented:

“[In the] years leading up to the First World War, the eugenics movement looked like a Darwin family business. ... Darwin’s son Leonard replaced his cousin Galton as chairman of the national Eugenics Society in 1911. In the same year an offshoot of the society was formed in Cambridge. Among its leading members were three more of Charles Darwin’s sons, Horace, Francis and George.”<sup>1,2</sup>

This continued well into the 20<sup>th</sup> century: “It was Darwinists (Huxley, Fisher, Dobzhansky, Muller, others)

who fueled the campaign for eugenics” (p. 159).

Eugenics is now only of historical interest. Or is it? The link between eugenics and evolutionary thinking is not completely gone even today. Princeton philosopher Peter Singer advocated that disabled human infants should be put to death, complaining that only the Christian had prevented this.<sup>3</sup> What about inconvenient children? Then two Italian philosophers also took so-called abortion rights to their logical conclusion in a prestigious medical ethics journal.<sup>4</sup> They seriously suggested that even healthy infants that have been born have no right to live, and should be killed if they are inconvenient to their family (p. 162).<sup>5</sup>

### Neo-Darwinism: an intellectual strait-jacket

In the 20<sup>th</sup> century, Darwinism, according to Bennett, was very resistant to new ideas, even ones that in no sense could bring God back into the picture. He lists several ideas that were slow to be accepted by the ruling Darwinian school of thought. He comments:

“Think of all the ideas put forth by Darwinists that proved entirely fictitious—blending, gemmules, the Wiesmann Barrier, the Central Dogma, kind selection, selfish genes, the Handicap Principle and many others. Even natural selection has little, if any, supporting evidence” (p. 200).

Bennett then elaborates on the many adaptationist just-so stories that have been told by Darwinists. However, according to the author, the problem with standard evolutionary thinking is much deeper. Bennett suggests that Darwinism adopted an excessively gene-centred view of evolution.

The gene-centredness of current evolutionary theory is exemplified by Richard Dawkins’ *The Selfish Gene* (1976). Non-conforming evidence



was explained away by auxiliary hypotheses. For instance, altruistic behaviour in nature was attributed to kin selection. As an example, it is adaptive for an individual bee to give its life in defense of the hive, because the bee's genes will then live on through the physical survival of the other bees in the hive. The author asserts that no evidence has been found to support kin selection, but much evidence has accumulated against it. For instance, African army ants regularly attack and cannibalize their own.

[However, I can think of a counterargument: the survival of the cannibal ant individual is adaptive because its genes get passed on, even if this takes place at the expense of one's siblings. From an evolutionary standpoint, it is better that one set of genes survive than no cannibalism takes place and thereby *no* set of genes survive. This brings us to a more fundamental issue: if a theory cannot be falsified, it is not scientific, according to the Popperian criterion. Since any possible observation could potentially be reconciled with kin selection, how would one know that kin selection is false?]

### **So-called self-organization—an assumption, not fact**

The author spends the latter part of his book rolling out a completely new theory of evolution—one based on supposed self-organization of matter and of living systems.

In fact, author Bennett portrays self-organization as something inherent in matter—something that makes stars out of gas, galaxies out of stars, etc. Bennett is clearly using 'self-organization' as an evolutionary cover word. He is begging the question with a vengeance, by assuming the very thing he needs to prove. Thus, he is assuming that gas spontaneously organized itself into stars, etc., despite the enormous difficulties.<sup>6</sup> Then he closes the circle of reasoning by saying

that the spontaneous organization of gas into stars etc. demonstrates the inherent self-organizing properties of matter.

The author discusses what he calls 'emergent properties'. These are novel capabilities that have not existed in an earlier state of organization, but now emerge as a result of the association of units. For instance, he cites the surface tension of water, which, he claims, is an emergent property, in that (to him) it was not a property inherent to the water molecules themselves. However, surface tension results from the hydrogen bonds, and these most certainly act at the molecular level. Thus, surface tension (and other unusual properties of water—such as the high boiling point relative to molecules of comparable low molecular weight) is a property that occurs at the molecular level.

The issue, however, is more fundamental. As with so-called self-organization, Bennett uses 'emergent properties' as a buzz phrase that begs the question about its origins.

### **Living things are not ruled by genes**

The author refutes the 'genes specify everything' mindset of much of conventional evolutionary thinking. For instance, he shows that the social behaviour of ants and bees is determined neither by genetically imposed instinct nor by the governing influence of the queen—a governing influence that, unlike that of the human queen, is non-existent. Instead, the tendency to do specific jobs in a hive or colony is governed by the interaction dynamics of the individuals.

In like manner, ontology is governed less by commands from genes and more by the interaction of the developing embryonic entities. In a fascinating quoted experiment, a group of individual retinal cells assembled themselves, *in vitro*, into an optic-cup

structure, and did so in the absence of a lens.<sup>7</sup>

The foregoing discussion revolves around the subject of biological information. However, whether biological information resides in genes, interacting cells, interacting tissues, or interacting creatures, is not as crucial as the *origin* of this biological information. Did it arise from blind, natural processes, or can it be explained only by a designer?

### **Evolutionary storytelling: old and new—in a nutshell**

Bennett's mentality is unoriginal. He follows the standard question-begging line of "Living things exist; therefore organic evolution must have happened."

Let us now summarize, and contrast, the conventional and new ideas of evolution. When referring to the giraffe's long neck, the conventional evolutionist says, "Genetic mutations, edited by ongoing natural selection, made it that way", and then proposes an evolutionary adaptationist tale to speculate how it took place, such as the one about the longer-necked giraffe able to reach otherwise out-of-reach leaves to eat. Were Bennett applying his ideas to the origin of the giraffe's long neck, he could say, "Relatively rapid, environmentally stress-driven changes in the silencing and expression of genes, acting within the constraints of developmental pathways, made it that way." He then could engage in his own version of storytelling, spinning a tale about the neck area of the ancestral giraffe embryo undergoing accelerated and/or unchecked growth, leading to the exaggerated neck.

### **A comeback for embryonic recapitulation**

Throughout this work, the author downplays the role of genes in evolution and emphasizes the interaction of biological units during development.

He adopts an ‘add-on’ model of general evolution. According to this concept, major evolutionary changes involve the addition of a new ‘layer’ of sequential physical relationship over the pre-existing ones, rather than the restructuring of previous modes of existence. It is for this reason that so-called atavistic structures sometimes reappear, and ontogeny (supposedly) recapitulates phylogeny (figure 2).

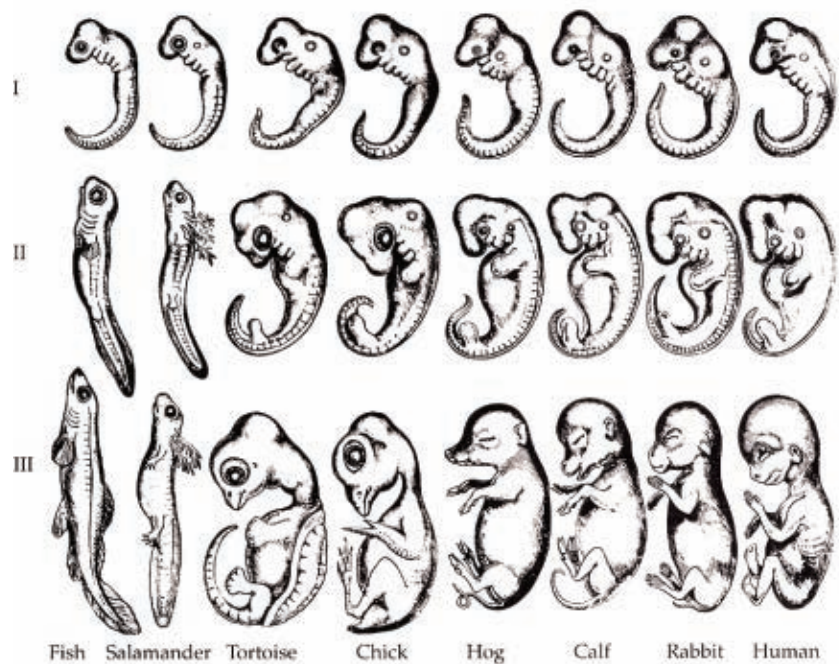
The author takes the atavistic-structure argument further. He cites some experiments, including one that supposedly caused the appearance of an ancestral, dinosaur-like mode of tail development in modern birds. However, it is unclear what the perturbations in development, whether experimental or natural, really mean. For instance, six-fingered humans sometimes are born, but no-one suggests that this is an atavism, because humans are not believed to have ever had six-fingered ancestors.

As for the embryonic recapitulation theory, is it not one that has been discredited a long time ago?<sup>8</sup> In any case, it is rife with special pleading. For example, if humans go through a ‘fish stage’, as manifested by the pharyngeal pouches (‘gill slits’), then why no scales, slimy skins, piscine-like tails, etc. in the embryo? Oh well, these must (conveniently) have been lost.

### Evolution: too fast and too slow to be seen

The author touches on alleged simultaneous evolutionary changes in organisms, and dusts off Richard Goldschmidt’s ‘hopeful monster’ conjecture. However, as with the original idea, it is based solely on evolutionary hope, and is devoid of supportive evidence.

Author Bennett unreservedly appreciates the discontinuities seen among fossils, notably in the Cambrian explosion. He even cites the failure of so-proclaimed transitional forms. For



**Figure 2.** The long-abandoned embryonic recapitulation theory is revived according to the arguments presented in this book.

instance, ocean-dwelling flatworms were thought to be transitional between primitive and complex animals until they were found to have the same genes as complex animals (p. 269).

The author revives the idea of punctuated equilibrium, and does so with a twist. He suggests that stasis customarily exists among organisms because their organismic organization is resistant to destabilization. However, once destabilization advances beyond a certain level, the stasis breaks down, and there is supposedly a rapid burst of evolutionary change, leading to a new stable and resistant-to-change configuration. That, to him, is how new species come into existence.

As an example of stasis, disequilibrium, and a novel stasis, he brings up the example of a pile of sand. One can keep adding sand grains, and nothing happens. However, there comes a point when adding another grain of sand causes the pile to suddenly collapse. After that, there is a new, stable layer of sand. This analogy is superficial at best and useless at worst.

The stability of the original sand pile exists only because the force of friction between the sand particles is greater than the force of gravity that is acting on the sand particles to get them to slide past each other. One excessive sand grain, and the force of gravity is now greater than the resistive force of friction, and the pile collapses. There is nothing remarkable in that, and it has absolutely nothing to do with any hypothetical reorganization of living things and emergence of new species.

It is clear that Bennett is not advancing anything new. All he does is return us to the time-worn theme that evolution, conveniently, occurs too slowly to be seen in real life, and also too fast to be seen in the fossil record.

### Still no role for God

Bennett claims that his ideas reconcile God and evolution. They do not. All versions of evolution repudiate *any* form of divine intervention, purpose, or supervision. All of them rely on blind, natural processes—only

different ones—to supposedly produce order from disorder, life from non-life, and new, more complex forms of life from preceding, less complex forms of life, etc.

Let us return to the subject, raised by Bennett, of emergent properties. As noted earlier, Bennett has performed a bait-and-switch, confusing the existence of emergent properties with the (imagined evolutionary) origin of emergent properties. To extend this consideration, let us think of the watch and the jet plane. Both are made of metal. The ability to tell time and the ability to fly are clearly emergent properties, as neither ability is in any way a property of any metal. The ability to tell time and the ability to fly are the outworking of a specific configurational entropy (or specified complexity) that has been imposed upon the metals. No blind, natural process can impose this specified complexity upon the metals. Only an intelligent designer can do that. Now if this is so obviously true of the emergent properties of relatively simple man-made devices, how much truer is it of the vastly more complex emergent properties of living things?

### Watch out for the creationist bogeyman!

Any questioning of evolutionary dogmas has been made taboo, even if the questioning was done by evolutionists working in a strictly evolutionistic framework of thinking. Bennett comments, “Despite this, any scientific criticism of Darwin was branded ‘anti-evolution’ and ‘creationist’. Defending Darwinism became synonymous with defending science [emphasis in original]” (p. 200). [What else is new?]

In fact, Bennett describes the bitter infighting among evolutionists on matters of disagreement (pp. 358–362). It takes on comical proportions. In fact, any evolutionist who questions conventional evolutionary claims

is attacked as a ‘creationist helper’ (p. 198).

### Implications for creationist research

The silencing of genes accounts for the blindness of cave fish. This solves the apparent problem of God creating fish with non-functional eyes. He didn’t. Clearly, this blindness is ephemeral. In fact, the breeding together of blind cave fish, from different caves, compensates for the independent silencings, causing the progeny to have normal sight (p. 302).<sup>9</sup> This also shows that this blindness must have arisen recently. Without selection pressure of *needing* sight, the genes for sight would have been irreparably damaged by random mutations over many generations.<sup>10</sup>

In my detailed work on Noah’s Ark,<sup>11</sup> and the aftermath of the Flood, I identified changes in the animals’ genomes that can help us understanding the marked and rapid changes in the descendants of the animals released off Noah’s Ark, including the origin of new species from the genus-kinds (or family-kinds) on the Ark.

Bennett updates the subject of rapid changes. Darwin’s famous Galápagos Island finches are instructive. Major changes in the beaks can occur within a few generations, much too quickly to be explained by natural selection. We now realize that the environmental stress of a changed diet ‘unsilences’ the finches’ genes that govern the development of the beaks, thus driving the ‘overnight’ changes.

### Conclusions

This work is yet another one by an evolutionist who admits that existing theories of evolution are completely inadequate. However, the new version of evolution is no less conjectural than the old one. The creationist can agree with each evolutionist about the

inadequacy of the other’s evolutionary model.

The silencing and ‘unsilencing’ of genes, and the effects of environment on genetic expression, is of broad-based interest. It can help account for the rapid diversification of life, from a few founders, after the Flood, in a matter of a few thousand years or less.

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# Mixing Darwin and the Bible damages ecological theology

***Ask the Beasts: Darwin and the God of Love***

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Bloomsbury, London, 2014

Shaun Doyle

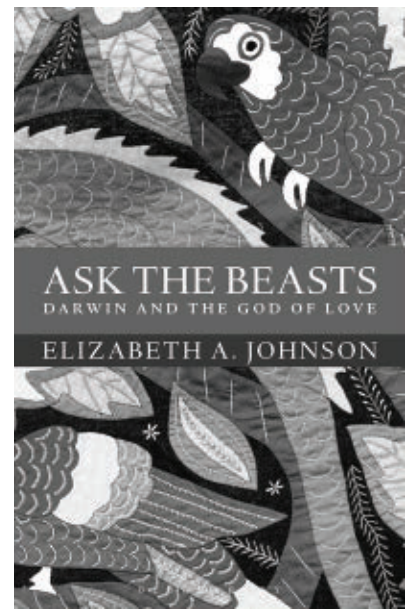
The environmental debate is a hot topic and has suffered somewhat under the ‘coercive consensus’ mentality that is so familiar to biblical creationists in the origins debate. This book brings together those two worlds as it tries to triangulate them with the Bible to provide what we might call an ‘evolutionary ecological theology’. In light of the continued debate among biblical creationists on the nature and urgency of our ecological task,<sup>1</sup> I will generally refrain from entering that debate. Rather, I will pay special attention to the role of evolution in this attempted triangulation of evolution, ecology, and the Bible. Evolution is the weak link that, as is well known to biblical creationists, undermines biblical theology, but I will argue that it also damages the Christian ecological vocation regardless of how one views the nature and urgency of the ecological task.

The author Elizabeth Johnson (b. 1941), is a member of the Sisters of St Joseph, a Distinguished Professor of Theology at the Jesuit Fordham University (NY), and a well-known feminist theologian.<sup>2</sup> The book’s title comes from Job 12:7: “Ask the beasts and they will teach you.”

## Ode to Darwin

The early chapters are devoted to an ‘exposition’ of Darwin and Darwinian evolution, though a more fitting description may be ‘celebration’. First recounting his life with fervent appreciation, Johnson documents Darwin’s descent from Christianity into agnosticism. But the main value she sees in Darwin is his ‘ascetic’ devotion to the study of nature (p. 42). There is little note of warning in her recounting of Darwin’s saddening ideological trajectory through life (motivated more by the death of his loved ones than by his study of nature). For Johnson, Darwin is basically a ‘friend on a parallel road’ who can even act as a moral exemplar for *Christians!* However, there is nothing exemplar about Darwin’s rejection of Christianity. Moreover, even his practically idolatrous appreciation of nature, which Johnson is at pains to praise Darwin for, seemed to be stifled by his agnosticism in later life: “In later years, sadly, he wrote that even the beauty of the natural world ceased any more to awaken his admiration” (pp. 39–40).

Second, Johnson offers a eucharistic summary of Darwin’s *magnum opus* *On the Origin of the Species*. There is little to say about it that hasn’t been said in *Journal of Creation* (and plenty of other creationist venues) before. We see the standard depictions—natural selection as a quasi-omnipotent hypo-stated force capable of bending biology in almost any way conceivable; an unwarranted *a fortiori* argument from selective breeding to natural selection; the little blind watchmaker



that could ... given enough time; and, the evolutionary ‘tree of life’. Johnson does however inadvertently point out that Darwin never tried rebutting biblical biology. Darwin’s main foil was not Moses but Lyell—who held to a type of intermittent creationism trapped in a notion of fixity of species that flew in the face of simple biogeography.

Johnson’s final task in ‘celebrating Darwin’ is to trace the history of evolutionary thought subsequent to the publication of *On the Origin of Species*. All she really does is present a reasonably shallow apologetic for neo-Darwinism. She extols the explanatory virtues of neo-Darwinism as filling in the ambiguities and fixing the deficiencies of Darwin’s basic idea. It’s interesting to see the way modern discoveries have ‘updated’ Darwin’s ideas to the point where Darwin is now basically irrelevant. Darwin’s ‘slow and steady’ changes has been replaced with a ‘sporadic, speedy, and mostly static’ model driven by catastrophes—punctuated equilibrium. It’s also interesting to see how this ‘update’ to Darwin’s ideas is soberly propounded as true alongside the notion that palaeontologists have filled in many

gaps in the fossil record of evolution. Punctuated equilibrium is based on the paleontological fact we *don't* see such a plethora of missing links in the fossils.<sup>3</sup> This doesn't demonstrate the success of Darwin's ideas; it demonstrates how malleable the core idea of naturalism applied to biology really is.<sup>4</sup>

Johnson then places biological evolution in its broader context—the big bang history of the universe. Again she waxes liturgical—she extols the beauty of this open-ended picture. For her, evolution is the drumbeat of the cosmos—intensely situational, yet with a seemingly innate tendency to complexify. It seems that someone forgot to tell her that we've never observed tornadoes in junkyards smash together 747s—nature does not spontaneously self-complexify in the way she needs it to.<sup>5</sup>

### Theological issues

Where is the Father?

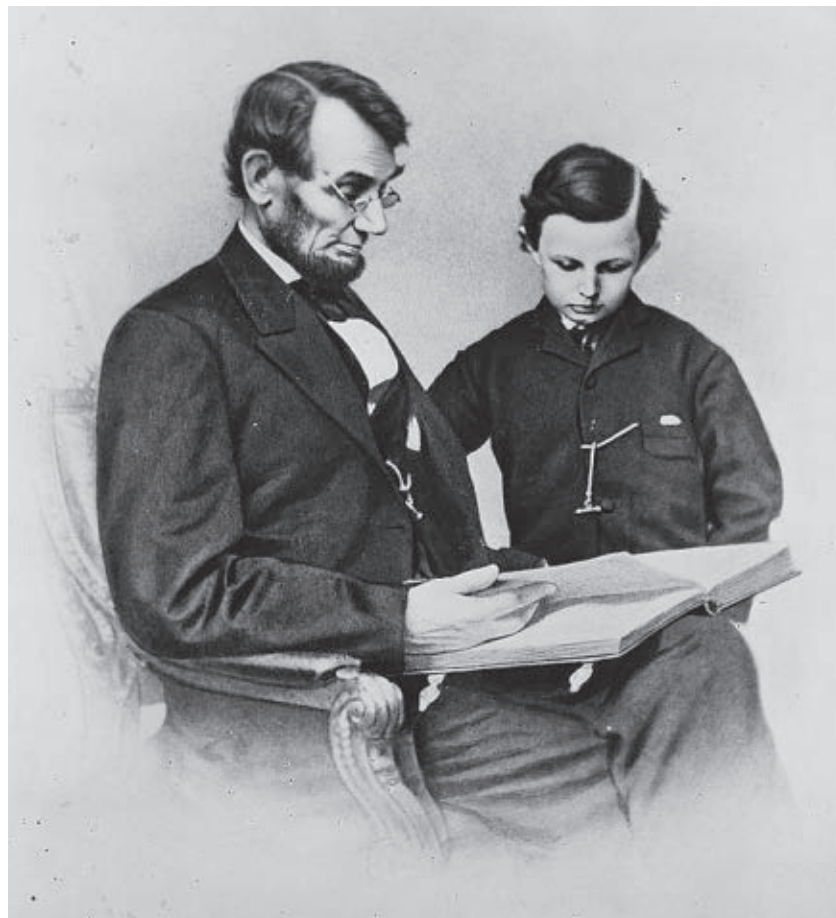
Johnson has a very strong disdain for 'patriarchal androcentrism'. It is one of the three main 'obstacles' she sees to building a 'healthy' eco-evolutionary theology (the other two being different forms of hierarchical substance dualism; pp. 125–128). She accuses it of working in concert with hierarchical substance dualism by associating men with 'spirit' and women with 'matter', thus making men more valuable than women. This patriarchy apparently "can turn violent and exploitative with little compunction" (p. 126).

We can indeed agree that man-centred patriarchy has caused many problems. For the sake of argument, let's even grant that patriarchal androcentrism has been as bad for environment and society as Johnson says. Nevertheless, this still says little about paternity or patriarchalism *per se*. Moreover, the Bible clearly rejects

the notion that *all* forms of patriarchy are bad, since one of the most dominant positive theological motifs of the New Testament is patriarchal *theocentrism* (cf. e.g. John 12:28, Philippians 2:11, Ephesians 3:14–15, and James 1:18). What does Johnson have to say about this? How might we reform and reformulate the notions of patriarchy and paternity along biblical lines to provide us with rich theological impetus for the ecological task?

Despite being so vocal about the problems patriarchy has caused, she offers *nothing* on how to reconceptualize patriarchy as part of the solution. The references to Jesus and the Spirit run into the hundreds throughout the book but there are only nine references specifically to the

Father. She develops a rich and nuanced ecological theologies of Christ and the Spirit but offers nothing towards a positive ecological theology of the Father. She frequently discusses 'God', and where a specific divine person is the intended reference, it would most naturally refer to the Father. But there is a world of semantic difference between calling the first person of the Trinity 'God' and calling *him* 'Father' when patriarchy is a major target for criticism. For instance, she glosses over a rich picture of *paternal* care in Luke 12:6 for a more generic focus on *theological* care, and one that focuses on the care of Jesus and the Spirit when the explicit subject of the passage is the Father (pp. 233–234)!



Johnson's dismissal of patriarchy mirrors her silence on the Father in her 'Trinitarian' ecological theology, and thus lacks any notion that *paternal* care could contribute positively to our understanding of the ecological task."

It's hard not to be left with the impression that Johnson thinks patriarchy is irredeemable; it can only be part of the problem and can't offer anything to the solution. This is to be expected from someone who was described as "one of those hard feminists who think that the use of that label [patriarchal] is enough to settle a debate".<sup>6</sup> Thus the absence of the Father from her positive theologizing is a massive lacuna, especially in light of the strident denunciation of patriarchy as manifested among men. After all, if anyone can offer a theological impetus to our ecological behaviour, surely the Father can, since not even a single sparrow is forgotten by Him (Luke 12:6).

#### Panentheism?

Another theological problem is Johnson's 'panentheism'. Classically defined, 'panentheism' means that the world is a part of God, such as is found in neo-Platonism and process theology. This blurs the ontological distinction between God and the world (figure 2), and is a blatant denial of God's transcendence and *creatio ex nihilo*. But is this what Johnson means? She defines 'panentheism' as 'all is in God', but this is vague; both classical theists (Acts 17:28, cf. Acts 17:24–25) and classical pantheists can use this

language. She tries to clarify what she means by taking 'in' in an 'ontological sense', which sounds like classical panentheism. However, she actually *affirms creatio ex nihilo*!

"... 'out of nothing' means that God creates but not *from* anything else. ... God's creative act ... presupposes nothing except the power of divine love which brings into existence something to be worked on in the first place" (p. 216).<sup>7</sup>

What's with this conceptual confusion? Olson believes 'panentheism' is being extended beyond its classical definition.<sup>8</sup> He notes a number of self-styled 'Christian pantheists' who are using the term 'panentheism' as a cipher to emphasize the intimacy of relation between God and the world. As such, Olson rightly argues, they are emptying the term of any meaningful theological content.

#### Suffering evolution

Johnson also accepts that pain,<sup>9</sup> suffering, and death are integral to the evolutionary process, and that any Adamic explanation for the origin of death and suffering in the world is inconsistent with theistic evolution (pp. 184–185). Instead, Johnson appeals to the 'freedom' of creation to

essentially get God 'off the hook' for the evils of evolution:

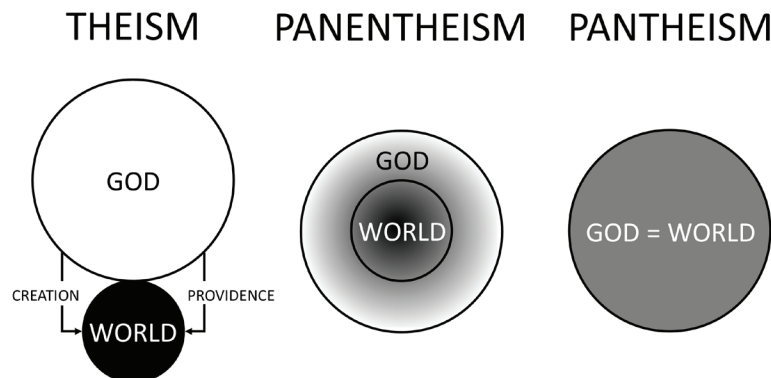
"Affliction arose from below, so to speak, rather than being imposed from above by direct divine will. Theologians are wont to call this the 'free process' position. Similar to discussions of free will, which is given to human beings by God yet used at times to oppose the divine will, free process in nature works in ways not necessarily always according to divine design" (p. 191).

But what does this 'freedom' actually entail? Dembski eloquently points out an irony in such 'free process' ideas:

"How can the freedom of creation, which results from a freely acting God who freely bestows freedom on creation, *force* us to become sinners and *force* the world to be a dangerous place full of natural evil? Shouldn't the freedom of creation rather give us freedom *not* to sin? And shouldn't it be possible for God to create a world whose freedom is not destructive and does not entail natural evil? Such theodicies of freedom require, at crucial points, the sacrifice of freedom."<sup>10</sup>

But worse, this free process view makes God weak, ignorant, or sadistic. Johnson clearly wants to avoid a sadistic or indifferent God:

"What John Paul II calls 'the pain of God in Christ crucified' places the living God in solidarity with all creatures that suffer in the struggle of life's evolution. This unfathomable divine presence means they are not alone but accompanied in their anguish and dying with a love that does not snap off just because they are in trouble. Biologically speaking, new life continuously comes from death, over time. Theologically speaking, the cross gives grounds to hope that the presence of the living God



**Figure 1.** Classical panentheism locates the world ontologically inside God and blurs the distinction between the two. In contrast, in theism God is distinct from the world but remains in contact with it (in order to sustain it and interact with it), and pantheism equates God and the world.



in the midst of pain bears creation forward with an unimaginable promise” (p. 210).

And rightfully so. However, that leaves us with a weak and/or ignorant God, given theistic evolution. Didn’t God know that these natural laws, left to their own devices, would produce billions of years of death and suffering? It’s not hard for us to notice, so surely God would’ve picked up on it! Or is God incapable of controlling the beast he unleashed on us? Then why would he have unleashed it in the first place? Remember that, according to theistic evolution, the world was *made to be* a death-filled place; it was not *subjected* to futility as a result of sin (Romans 8:20–22). As such, even Jesus’ death and resurrection don’t provide any comfort, because not even that guarantees that God can set everything right. Sure, he can save his Son, but what about the rest of us? If the world does things outside of God’s control, then there’s no guarantee that God can overcome the evil in the world.

But Johnson does indeed want to affirm an ecological eschatology of hope: “To my way of thinking, a case can be made that for God to love the whole means to love every part. Hence to save the whole means to save every individual, every bear” (p. 230). But she also said: “To be created is to be finite and mortal. Such limitation is not evil but simply the condition of being a creature” (p. 219). This is contradictory; if death is intrinsic to created being, then we cannot hope for a deathless future. We will always be creatures, and as long as “To be created is to be ... mortal”, then we *must* be mortal.<sup>11</sup> Moreover, this not only presumes that theistic evolution is true but that God *had* to use evolution to create, which is absurd. God was free to specially create creatures that could live forever.

Nonetheless, Johnson’s ‘ecological eschatology’ may strike many as overly sentimental but the general picture she paints is not without

support in church history. She rightly castigates a trajectory of thought that devalues the redemptive value of the non-human living world, taking e.g. Thomas Aquinas<sup>12</sup> to task for excluding animals and plants from the new heavens and earth (p. 229). And she draws support for her view from John Wesley (commenting on Romans 8:19–22) that all individual creatures will be redeemed:

“In the new earth, as well as the new heavens, there will be nothing to give pain, but everything that the wisdom and goodness of God can create to give happiness. As a recompense for what they once suffered while under ‘the bondage of corruption’ ... they shall enjoy happiness suited to their state, without alloy, without interruption, and without end” (p. 232).<sup>13</sup>

However, note the crucial phrase for Wesley’s belief in the final redemption of all animals: “As a recompense for what they once suffered while under ‘the bondage of corruption’”. For Wesley, this was *not* a condition animals were created in, as theistic evolution maintains, but was a consequence of the Fall:

“As all the blessings of God in paradise flowed through man to the inferior creatures; as man was the great channel of communication, between the Creator and the whole brute creation; *so when man made himself incapable of transmitting those blessings*, that communication was necessarily cut off [emphasis added].”<sup>13</sup>

A rebellious world for rebellious man. The world reflects the state of its steward. The Bible is clear that human mortality and creaturely corruption resulted from Adam’s sin and thus were not necessary (Genesis 3:19, Romans 5:12, Romans 8:19–23, and 1 Corinthians 15:20–22). Theistic evolution *cannot* operate under such a rubric because death and suffering are *intrinsic* to evolutionary process but this is quite clearly contradicts the rubric of

Romans 8:19–22.<sup>14</sup> As such, Johnson finds herself agreeing with Wesley’s ‘eco-eschatology’ while jettisoning the only framework able to justify it from Scripture—biblical creation.

### Evolutionary ecotheology?

So how does Johnson try to draw evolution and biblical theism together to reform our thinking about ecology? Her first notion is a ‘conversion to the Earth’: “Facing these evils in a spirit of repentance, we need the grace to be converted to the patterns established by the Spirit in the giving of life itself. We need a deep spiritual conversion to the Earth” (p. 258). To do that, Johnson says we need a new paradigm to view the Earth through—the community of creation paradigm, which “positions humans not above but within the living world which has its own relationship to God accompanied by a divinely-given mandate to thrive” (p. 267). She says that the old ‘dominion paradigm’ of Genesis 1:28 and Psalm 8 apparently ended up facilitating all the sins that have brought about the ‘ecological crisis’. She applauds attempts to reform the paradigm along the lines of stewardship (p. 266), but they’re apparently still not enough:

“The strong hubris entailed in the effective history of this paradigm needs to be remedied by a different conceptuality of the human place in the world, religiously speaking” (p. 267).

This is too hasty. We can turn this back on Johnson’s ‘community’ paradigm just as harshly—since community members can be lazy freeloaders, perhaps we should abandon the community paradigm altogether! If there is any problem with the dominion paradigm, it’s not that it’s inherently flawed, it’s that it’s *incomplete*. But so too is the ‘community of creation’ paradigm. The fundamental lack in the community of creation paradigm is that, in itself, it doesn’t delineate what role we should have in that

paradigm. There are many different roles in a community, but in a *human* community most of those roles come with *responsibilities* concomitant with our moral abilities. However, in the ‘community of creation’ *only humans* have any real responsibilities within the ‘community’; the rest of the biosphere just does what it will.

She struck a better balance earlier in the chapter: “When interpreted as a whole, the Bible situates the function of dominion within a broader vision of a community of all living creatures centered on God” (p. 262). And yet, one still gets the distinct impression that the notion of *authority* does not sit well with Johnson. This would explain the lack of attention to the Father alongside the vehement denunciation of patriarchy, and it would also explain her ambivalent approach to the dominion paradigm—it’s clearly in the Bible, so she can’t just jettison it, but she clearly doesn’t like it either. But again, there are biblical resources that would’ve allowed her to reformulate the notion of authority rather than ignoring it, e.g. Mark 10:35–45, John 10:1–18, and 1 Peter 5:1–4. Just because authority and paternity can be abused doesn’t mean they can’t be properly used, even for the ecological task.

At any rate, where does evolution figure into this discussion? The main positive contribution Johnson sees it having is the extended notion of ‘family’ that evolution entails: “we are all kin in the evolving community of life now under siege” (p. 285). But that is not fundamental to even Johnson’s picture: “When parsed to its most basic element, the relational pattern of the community of creation is founded on the belief that all beings are in fact creatures, sustained in life by the Creator of all that is” (p. 268). And why do we need evolution to convince us that all beings are God’s creatures? If history teaches us anything, it’s that evolution *obscures* this belief because it attributes the origin of creatures purely to natural processes—a ruthless struggle for

existence that eliminates the unfit. As such, any benefits that might come from the ‘familial’ rubric of evolution are more than offset by how it obscures the doctrine of creation. At any rate, the discussion of ecological vocation can proceed completely without reference to evolution, as shown by the very same sorts of discussions taking place among biblical creationists!<sup>1</sup> Evolution is at best irrelevant and at worst positively detrimental to the ecological discussion.

### Conclusions

Evolution doesn’t help either theology or ecology. The most it can ever achieve is to provide us with a cheap sentiment of ‘family’. However, that doesn’t even compare to the theological power of the doctrine of creation, a doctrine which evolution *obscures*. It gives rise to either a harsh deism where God doesn’t care, or a sentimental pantheism where God cares so much but can’t do anything about it. Both are but a hair’s breadth from atheism. Johnson is definitely closer to the pantheistic road, which fits our zeitgeist. It tells in her sentimental ‘pantheism’, but perhaps most poignantly (and ironically) in the absence of the Father from her theological picture. The Father is transcendent and the source of all authority; two things Johnson does not give much attention to, and even denigrates, in the case of authority. We need the Father’s care as much for the ecological vocation as anything else, but Johnson ignores His particular voice. Evolution also blunts our emotive response to the suffering of creation; evolution has creation suffering because God made it to suffer, rather than as a result of *our* sin. If creation’s plight is our fault *in toto*, then it provides a great emotional impetus to do what we can to alleviate its suffering. If it’s not, our hearts can become calloused toward God *and* creation, regardless of how else we

might describe them. The fundamental problem? Evolution is *false*; framing our vocations around false ideas and ideals will distort and destroy any good we hope to achieve.

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7. Johnson follows Thomas Aquinas in allowing that *creatio ex nihilo* is consistent with an eternal universe (p. 217), which is a disputed position in church history, but orthodox. But unlike Thomas, she rests her views squarely on ‘science’ (big bang theory) rather than Scripture (Genesis 1:1, John 1:1–3, etc.).
8. Olson, R.E., A postconservative evangelical response to pantheism, *Evangelical Quarterly* 85(4):328–337, 2013.
9. It’s important to note that our physical pain sensory system did *not* arise as a result of the Fall, but we were created with it. For more information, see Speck, P.L., Pain and the Adam bomb; in: Ivey, R.L. Jr, (Ed.), *Proceedings of the Fifth International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 457–464, 2003.
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11. Theistic evolutionists typically won’t accept this, mostly because (if they believe in the historical Incarnation, death, and resurrection of Jesus) they usually want some sort of traditional eschatology. But if resurrection and eternal life are our future, then mortality is clearly not intrinsic to creatureliness. This also raises the question: why would God create us bound in mortality when Genesis 2:17, 3:19, and 3:22 together portray *physical* death as a consequence of sin?
12. Thomas Aquinas, *Summa Theologica* III (Supplement), q. 91, a. 5. Johnson rightly notes: “while this part of the *Summa* was composed after Aquinas’ death by students who drew on his teaching to complete the work, it is taken to be a fair representation of his thinking” (p. 301).
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# Adam's Day

## ***Reading Genesis 1–2: An Evangelical Conversation***

J. Daryl Charles (Ed.)

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Ting Wang

**I**t is not necessary”, contends Tremper Longman, “that Adam be a historical individual for [Genesis 1–2] to be without error in what it intends to teach” (p. 122). “If the first Adam is not really historical”, Todd Beall responds, “then how can we insist that the second Adam is?” (p. 135).

*Reading Genesis 1–2* is structured as a written ‘conversation’, with each of five evangelical scholars contributing a chapter on Genesis 1–2, as well as responses to the other four views. Todd Beall masterfully advances the traditional plain-language view of Adam and creation while the other four scholars advance non-traditional views forged from some composite of authorial intent, audience relevance, scientific (particularly genetic) conclusions, ANE parallels, genre studies, and/or analogical days. Richard Averbeck advocates a ‘schematized’ interpretation of Genesis somewhat akin to that of the Framework hypothesis, C. John Collins analogical days, Tremper Longman III a figurative view of Genesis 1–2 based on the Framework hypothesis, and John Walton a non-material, ‘functional’ understanding of creation. Editor J. Daryl Charles provides the Foreword, Victor Hamilton the Introduction, and Kenneth Turner and Jud Davis round out the volume with contrasting ‘reflective essays’ on the theme ‘Reading Genesis Now’.

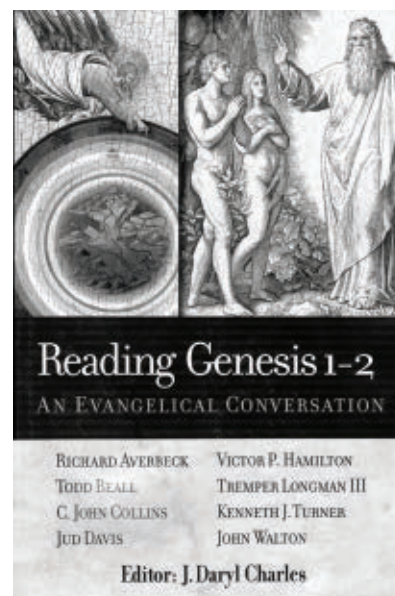
## **A brief synopsis of the seven chapters**

Richard Averbeck—“A Literary Day, Inter-Textual, and Contextual Reading of Genesis 1–2”

Averbeck recognizes that “there are good substantial reasons for reading Genesis 1 to refer to six literal days of creation and a seventh day of rest” (p. 7), and “for many years was satisfied with this reading” (p. 7), but he now contends that the literal view is “a misreading that does not properly allow for the genre and intent of the text and the figurative use of language” (p. 7). Instead, Averbeck now asserts that Genesis 1 is “schematized, not meant to be read in a literalistic way even by the ancient Israelites, and they would have known that” (p. 31), since “the author (whether we have the divine or the human author in mind) shaped the story of creation around what was observable and understandable to the ancient Israelites” (p. 8). This includes both the creation “backdrop” of the “deep, dark, watery abyss” (p. 12) as well as the “three-level universe” (heaven, Earth and subterranean waters/heaven, Earth, underworld/the three daughters of Baal) which “have parallels in the creation account in Gen 1” (p. 14). Indeed, Averbeck suggests that “the first set of three days in Gen 1 corresponds to the names of Baal’s three daughters” (p. 14). Although Averbeck recognizes “a necessary structure and sequence” (p. 31) to the six days of creation, he contends that “the seven days are not to be taken literally and are not intended to tell us how long God took in actually creating the cosmos or how old the earth is” (p. 31).

Todd Beall—“Reading Genesis 1–2: A Literal Approach”

Todd Beall asserts that “Genesis 1 should be read (along with all of Gen 1–11) as historical narrative that



is meant to be taken literally” (p. 46). In addition, there are structural and syntactic indications that “Gen 1–11 is to be understood in a similar way to Gen 12–50” (p. 47). Regarding ANE parallels, Beall points out that although “there are similarities between the biblical record in Genesis and ANE myths, there are far more significant differences” (p. 52). Indeed,

“... the Lord continually tells the children of Israel in the OT *not* to be like all the other nations in their worship of other gods, in their worldview. ... Far from following the thinking of the ancient Near East, Israel was told to reject it categorically [emphasis in original]” (p. 52).

Moreover, Beall points out that “time and again the NT writers refer to the details, not just the concepts, of Gen 1–11” (p. 54), and that “at least twenty-five NT passages refer to Gen 1–11, and all take the accounts literally” (p. 53). Beall contends that “many scholars propose nonliteral interpretations of Gen 1–2 in order to harmonize the biblical text with current scientific theory” (p. 56), and that “the continual teaching of evolution in public schools and universities for decades has taken



its toll. There is more evidence than ever against Darwinian evolution, but many evangelical scholars do not seem to be current on the subject” (p. 57). Beall concludes that “the simplest and correct approach to Gen 1–2 (as well as Gen 1–11) is to take it as a literal, historical account, just as Jesus and the NT writers did” (p. 57).

John Collins—“Reading Genesis 1–2 with the Grain: Analogical Days”

Collins asserts that Genesis 1–2 should be read “along its own grain” (p. 74) but also “as a part of a larger whole, that is, Gen 1–11” (p. 73). He views the purpose of Genesis 1–11 as providing “history without undue literalism” (p. 77) like the ‘prehistory’ (p. 77) and ‘protohistory’ (p. 77) of the Mesopotamians, who based “their stories on what they thought were actual events, albeit told with a great deal of imagery and symbolism” (p. 77). He understands the genre of Genesis 1 as ‘exalted prose’ (p. 83). Although Collins contends that Genesis 1–2 is one creation account and that “Gen 2 elaborates the events of the sixth day of Gen 1” (p. 82), he states that “the six ‘creation days’ are not necessarily the first actual days of the universe” or “necessarily the first days of the earth itself” (p. 85), and that based on Framework considerations (particularly Genesis 2:5), Creation Week lasted for “a year or longer” (p. 89). Regarding the meaning of Genesis, “we only need to consider how the farmers and nomadic shepherds who first heard this might have understood it” (p. 86), and “what Moses had in mind when he wrote Gen 1–2” (p. 90).

Tremper Longman—“What Genesis 1–2 Teaches (and What It Doesn’t)”

Longman contends that “the biblical text is not at all interested in telling us how God created the cosmos and humanity” (p. 103). Indeed, “the

absence of the sun, moon, and stars until the fourth day means that this pictorial description of creation as taking place during a week is not describing what actually happened” (p. 105). Longman views the creation account as structured as a ‘framework’:

“... the first three days of creation describe the creation of realms or habitats that are filled by the inhabitants of those realms in days 4 through 6, so that day 4 (sun, moon, and stars) fills day 1 (light and darkness), day 5 (birds and fish) fills day 2 (sky and sea), and day 6 (animals and humanity) fills day 3 (land)” (p. 105).

Regarding authorial intent, Longman writes, “it is important to recover the ancient context of a biblical text in order to understand its message according to its original intention” (p. 107). He views “two different accounts of creation” in Genesis 1–2, and states that “the most striking difference between Gen 1 and Gen 2 is in the area of the sequence of creation” (p. 108). Genesis “intends to teach us much about the nature of God, humanity, and the world, but not about how God created creation, including the sequence of creation” (p. 108). Indeed, “the intense use of obviously figurative language, the lack of sequence between the two creation accounts, and the text’s pervasive interplay with ANE creation accounts indicate that we are not getting a literal or precise depiction” of creation (p. 109). Longman, identifying himself as “an advocate of theistic evolution,” urges “responsible exegetes” to “go back and reconsider traditional interpretations in light of scientific discoveries and theories” (p. 121).

John Walton—“Reading Genesis 1 as Ancient Cosmology”

Walton asserts that “the Bible, though written for us and all humanity, was not written to us” (p. 141). In order to properly understand Scripture we must “understand the words

as an Israelite would have understood them; that we think of the cosmos the way that an Israelite would have thought of it” (p. 141). Indeed in Walton’s view, “the biblical author is approaching cosmology in a way that was familiar in the ancient world and not at all the way we would approach cosmology” (p. 152). From this perspective, “the interest of the text is functional throughout, with no interest in material origins” (p. 150). He contends that “Hellenism obliterated ANE ways of thinking” and, as a result, the “intertestamental literature, the NT, and writings of both the Church Fathers and rabbis all suggest a material understanding of Gen 1” (p. 157) erroneously. Walton also posits that “in Gen 1–2 the cosmos is viewed as sacred space [or temple] in which God rests” (p. 160).

Kenneth J. Turner—“Teaching Genesis 1 at a Christian College”

Turner observes that the controversy over Genesis has “only intensified since mapping of genome in 2001” (p. 188) and contends that “interfacing the Bible with modern science ... should be viewed as a hermeneutical issue not one about ultimate allegiance or authority”. In addition, “scientific understanding has rightly influenced re-examination and reinterpretation of several biblical descriptions” (p. 202). He states that in order to properly understand Genesis 1, “we must seek to enter the verbal and conceptual world of ancient Israel to find out how they spoke and thought about the interrelationships of deity, humanity, and the rest of creation” (p. 201). Nonetheless, with regard to Genesis 1, Turner writes: “Why would the moon be called a ‘light’ anyway, since we know from modern science that the moon only reflects the light from the sun? Why are the stars given a tertiary position? Isn’t the sun a star?” (p. 198). With respect to authorial intent, Turner asserts that

“the reader should assume that the human authorial intent approximates, or serves as the starting point for, the divine intent” (p. 200). In sum, “it is difficult to match the description and terms of days 1 and 4 with the world as we (and ancient Israel) know it, both phenomenologically and scientifically” (p. 198).

Jud Davis—“Unresolved Major Questions: Evangelicals and Genesis 1–2”

With regard to theology and exegesis in general, Davis observes that “everyone missed it before me” is a problematic position (p. 215) and that “there is no paleo-orthodox support for the view that Gen 1–3 should be interpreted to allow for long periods of time” (p. 216). Davis asserts that “if Jesus taught a view, I am bound to follow that view” (p. 211), and that “a *prima facie* case appears for understanding Jesus’ teaching: he

excludes the idea of the evolution of Adam and Eve from previous biological ancestors, and he positions their creation chronologically near the beginning of the universe” (p. 210; see figure 1). He concurs that “if therefore Christ was a historical individual, Adam himself must have been historical” (p. 213). Davis contends that any DNA similarities recognized by modern studies indicate a common Designer (p. 227). With respect to authorial intent, Davis notes a distinction between the “foreshadowed meaning” and the “initial meaning of Gen 1–2” (p. 230). For instance, “Gen 1–3 contains elements meant to foreshadow Christ and the new covenant” (p. 230) as revealed in Ephesians 5:31–32. Moreover, “is the chosen seed of the woman, which is initially Seth, meant [to the human author and the initial audience] to foreshadow the greater seed of Abraham and then ultimately David and even David’s heir, Christ?”

## Some recurring topics

### Genetics and genomics

“What is one to make”, Victor Hamilton inquires in the introduction to Reading Genesis 1–2, “of the conclusions of the mapping of the human genome project (under the direction of the cutting-edge scientist and evangelical believer Francis Collins) that the human race began with a colony of ten thousand and not with one male human and one female human?” (p. 3). Longman asserts: “Biologists now tell us that the origins of humanity do not go back to a single pair but rather to a breeding population of about ten thousand individuals. This conclusion raises the question of the historical Adam” (p. 121).

But how firm is this conclusion? The hypothetical breeding population of ten thousand derives from a landmark 1998 paper.<sup>1</sup> It is worth pointing out that the very first sentence



Figure 1. Michelangelo's "The Creation of Adam".

of the article after the abstract is: “When and where did humans evolve?” and that the methodologies and mathematical calculations utilize variables based on this assumption. Logically, the values chosen for the variables cannot prove evolution since they first presume it. As the first sentence demonstrates, the possibility of the biblical Adam is eliminated right from the gate, so it should not surprise us that the subsequent inferences, estimates, implications, and calculations yield a result entirely unfavourable to Adam. Even so, Longman posits that “the mapping of the human genome ... has produced, according to my Christian friends who are research biologists, overwhelming evidence in favor of evolution [emphasis added]” (p. 121). Let the reader note that the hypothesis of ten thousand breeders, rather than proving evolution, is itself founded upon evolutionary presuppositions.<sup>2</sup>

#### Copernicus

Although it is widely asserted that Copernicus proved empirically that the earth revolves around the sun, the simple fact is that he did not. Copernicus first assumed that the earth revolves around the sun, and then tailored his mathematical model to fit. As he points out toward the end of his monumental *De revolutionibus orbium coelestium*, “we have indicated to the best of our ability what power and effect the assumption of the revolution of the Earth has in the case of the apparent movement in longitude of the wandering stars and in what a sure and necessary order it places all the appearances”.<sup>3</sup> South African cosmologist George Ellis, in a 1995 *Scientific American* interview, asserts that:

“... people need to be aware that there is a range of models that could explain the observations ... For instance, I can construct you a spherically symmetrical

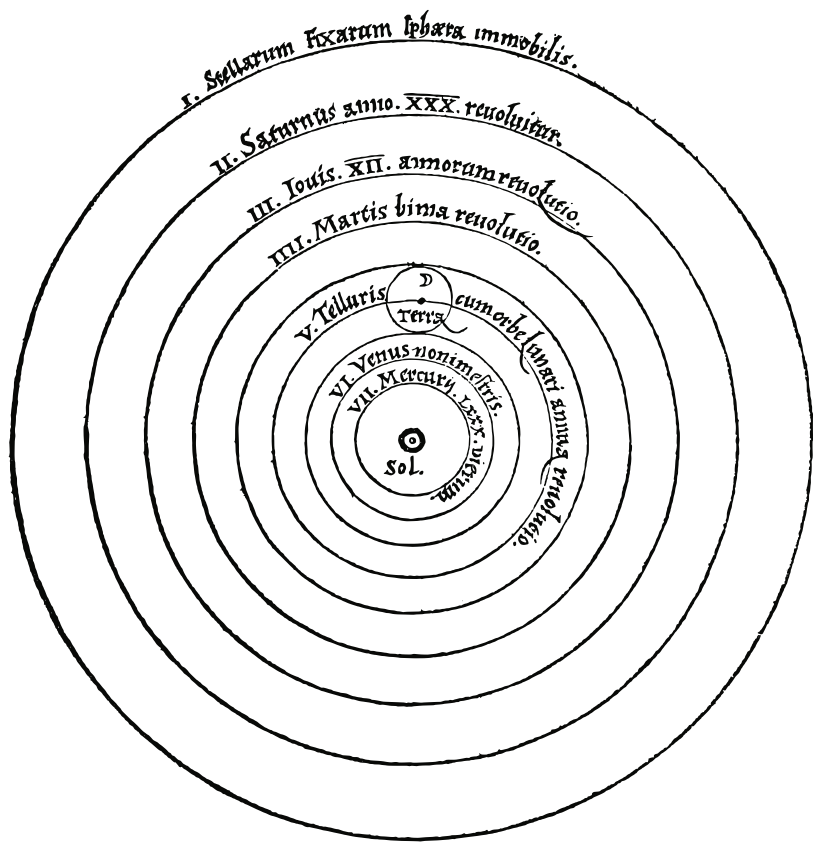


Figure 2. Copernicus' renowned heliocentric diagram.

universe with Earth at its center, and you cannot disprove it based on observations ... you can only exclude it on philosophical grounds. ... What I want to bring into the open is the fact that *we are using philosophical criteria* in choosing our models. A lot of cosmology tries to hide that.”<sup>4</sup>

Nonetheless, throughout *Reading Genesis 1–2*, Copernicanism is referred to not only as fact, but also occasionally as hermeneutical principle. For instance, Kenneth Turner, in his penultimate chapter “Teaching Genesis 1 at a Christian College”, regards Copernicanism “as a prelude and parallel to understanding the days of creation in Genesis” (p. 202, note 29). Similarly, Longman writes: “Everyone today recognizes the error of the church at the time of Galileo in constraining its scientists’ understanding of cosmology. Are we at a similar transitional moment

in connection to evolution?” (p. 129). Likewise, Walton writes: “Sometimes new advances in science do make us go back to the biblical text to see if we have been working on some wrong assumptions. Otherwise we would still believe that the sun revolved around the earth” (p. 72).

But let the reader note that, as Ellis indicates above, Copernicus’ cosmology has a philosophical rather than empirical basis. The ‘Copernican revolution’ was not, as Longman contends, an epochal instance of “science purifying religion” (p. 119), but rather the ascendancy of a particular philosophical worldview. It is plausible that Copernicus was deeply affected by the Hermetic writings that were first made available to Europe in Latin two years before he was born (these writings were extremely influential among the intellectuals of Copernicus’ day). It is worth pointing out that in



*De revolutionibus*, 1) Copernicus references Hermes Trismegistus (the latter name spelled without the first 's') reverently beneath the renowned heliocentric diagram (figure 2) and 2) Copernicus' heliocentric model matches the antecedent hermetic model *exactly*, from the sun unmoving at the very centre of the universe to the circular orbits, to the "sphere of the fixed stars". *Hermetica* XVI, written long before Copernicus' day, contends that "the sun is situated at the centre of the cosmos, wearing it like a crown"<sup>5</sup> and that "around the sun are eight spheres that depend from it: the sphere of the fixed stars, the six of the planets, and the one that surrounds the earth".<sup>6</sup> To my mind, this could amount to more than mere coincidence. Moreover, scientists from Hubble to Hoyle to Einstein to Hawking to Krauss have all admitted the overall lack of empirical, observational, and numerical proof for the Copernican position.

#### The Framework interpretation

Another recurring topic in *Reading Genesis 1–2* is the Framework interpretation, which derives from the work of Arie Noordtjiz in the 1920s.<sup>7</sup> The Framework interpretation regards the six days of Genesis 1 as a non-literal and non-sequential arrangement of creation events aligned topically within two parallel triads of figurative 'days'—rulers (days 1–3) positioned alongside realms (days 4–6). There are several exegetical problems with the hypothesis, among them that, as Beall indicates:

"... the so-called pattern between days 1–3 and 4–6 does not hold up well under scrutiny. For instance, the 'lights' of day 4 are put in the 'expanse' created on day 2, not day 1; the sea creatures of day 5 were told to fill the 'water in the seas' created on day 3, not day 2; and man was created on day 6 to rule over the land animals (also created

on day 6) and sea creatures and birds (created on day 5), not over the vegetation created on day 3" (p. 133).

Moreover, the plants mentioned in Genesis 2:5 (the verse which Meredith Kline considers the *crux interpretum* of the Framework interpretation and the "decisive word" against the straightforward reading of Genesis<sup>8</sup>) do not self-evidently comprise a merism (such as David's "when I sit and when I rise" in Psalm 139), which would represent all vegetation. Rather, the "shrub" (שִׁיחַ *sīach*) is a desert shrub (the word occurs not in Genesis 1 but three other times in the Hebrew bible, all in contexts of dessication and desperation) and the phrase "plant of the field" (עֵשֶׂב הַשָּׂדֶה *'ēseb hassādeh*) also appears not in Genesis 1 but rather next in Genesis 3 as a component of the curse upon Adam (and thrice more during the Exodus plagues upon Egypt). The terminology and phrasing regarding vegetation in Genesis 2:5 do not plausibly encompass the lush fruit trees of Genesis 1 and instead more feasibly describe certain post-Fall plants which recur in contexts of toil, anguish, and disaster. Lexically and contextually, it is likely that Averbek is correct in asserting: "These verses [Genesis 2:5–6] were meant to tell the Israelites that the conditions before the fall were not the same as after the fall. The struggle for existence that the curses in Gen 3 imposed was not a part of the original circumstances of humanity" (p. 29).

In addition, the Framework perspective on Genesis 2:5 necessitates that the first verb in Genesis 2:6 is translated with an 'inceptive nuance', such as: "So a rain-cloud began to arise from the earth. ..."<sup>9</sup> Mitchell Dahood considers 'rain-cloud' a 'tentative definition' based on his comparison of two calendars from Tel Mardikh/Ebla,<sup>10</sup> and implementation of this translation into biblical Hebrew includes understanding the preposition 'ל' (*le*) in Job 36:27 as 'from' rather than 'to'—which is

potentially problematic, but let us not digress. Kline explains that, "the first verb [in Genesis 2:6] is a Hebrew imperfect and the inceptive nuance—'began to'—is legitimate for that form and is *required* in this case if verse 6 is not to neutralize the first clause in verse 5b".<sup>11</sup>

But this translation requirement violates the principles of biblical Hebrew syntax, for the first verb of Genesis 2:6 occurs within a circumstantial clause (*waw* + noun + verb: וַיִּהְיֶה, which as Gesenius pointed out long ago, "always describes a state contemporaneous with the principle action" (§141e)—a conclusion not supplanted, but indeed strengthened, by subsequent investigations into ancient Semitic syntax. In other words, the biblical Hebrew circumstantial clause does not communicate 'so' or 'then' or 'next'—events logically/temporally subsequent—which would instead be expressed by the Hebrew narrative preterite. Nonetheless, the Framework perspective requires the circumstantial clause in 2:6 to denote *subsequent* rather than contemporaneous action, since in order to maintain the Framework exegesis of 2:5, there cannot already be water available for vegetation to grow. The Framework rendering of Genesis 2:5–6 conflicts with the foundational principles of biblical Hebrew syntax.

#### Genre

Also recurring throughout *Reading Genesis 1–2* is the question of genre. Averbek asserts that "Gen 1–2 constitute observational cosmogony and cosmology" (p. 31). Beall identifies Genesis as "narrative prose" (p. 49). Collins considers the creation account to be "exalted prose" (p. 83), whereas Longman opts for "theological history" (p. 110) and Turner for "doxological narrative" (p. 191). Walton asserts that "it is not important to label the genre (at least according to modern categories)" (p. 145), although he

considers Genesis to be “narrative” (p. 145) and “cosmology” (p. 145).

Genre theory is certainly not an ‘exact science’ and from ancient times it has been widely acknowledged that a text can simultaneously occupy more than one genre category—for instance, Aristotle considered the *Iliad* to be both epic and tragedy (*Poetics*, §24). With regard to Genesis, Beall points out that “there is no convincing genre category into which Gen 1 fits” (p. 62) and that “subjective genre definitions run the risk of assuming the conclusion and engaging in confirmation bias” (p. 177). In light of the Hebrew verbal syntax (Beall indicates that Genesis 1 contains 50 narrative preterites distributed among 31 verses), it is widely agreed by biblical scholars that Genesis 1–2 is narrative prose, but as Walton correctly points out, “proving it is narrative falls short of therefore identifying it is historical” and that even “as narrative prose, there are still a lot of genre options” (p. 70).

Nonetheless, Beall demonstrates exegetically that “Jesus and the NT writers” understood Genesis 1–2 “as a literal, historical account” (p. 57). To my mind, Beall’s discussion of New Testament views on Genesis 1–2 (pp. 53–56) is of exceeding importance and merits close study and reflection. As Davis astutely points out: “If Jesus taught a view, I am bound to follow that view” (p. 211). And yet, significantly, there is but one (!) New Testament citation in the four major non-literal chapters combined. I think that for proper biblical exegesis, it is crucial to remain consistent with what Scripture says about itself.

Instead, in some cases, the opposite seems to be true—for instance, in advocating his non-material view of Genesis creation, Walton writes: “I contend that Gen 1 has chosen to provide an account of functional origins, as would be typical in the ancient world, rather than an account of material origins,” but “a perusal of intertestamental literature, the *NT*, and writing of both the church fathers

and rabbis all suggest a material understanding of Gen 1, at least in part [emphasis added]” (pp. 156–157). Walton, it seems, is stating that his functional view of Gen 1 is correct and that the material (in part) view of the New Testament is incorrect. Let the reader be aware of the implications of such a position.

#### Audience relevance

Also recurring throughout *Reading Genesis* is the concept of ‘audience relevance’. John Walton asserts, “we must understand the words [of Genesis] as an Israelite would have understood them” (p. 141).

One obvious difficulty with this ‘relevance’ approach to Scripture is that we are simply not ancient Israelites, and thus any assertions as to what an ancient Israelite may or may not have known (insofar as these ideas are unexpressed in the biblical text) are speculative, and can lead to hermeneutical errors. For instance, Collins, in considering the use of the word ‘kind’ in Genesis 1, writes: “Now, the word ‘kind’ is not the same as ‘species’, nor is it even the question about whether one kind can turn into another. We only need to consider how the farmers and nomadic shepherds who first heard this might have understood it” (p. 86). But why are the farmers and nomadic shepherds all we need to consider? Surely God knew—indeed ordained—that his future people would also need Genesis to construct a worldview. Moreover, what if farmers and nomadic shepherds did sometimes wonder whether a sheep could give birth to something else?

Similarly, in defending his ‘analogy’ view of the seven days of Genesis 1, Averbeck writes: “The chapter is schematized, not meant to be read in a literalistic way even by the ancient Israelites, and they would have known that” (p. 31). But how does Averbeck know what the ancient Israelites would have known about schematization? In a similar way, John Walton, advocating

his view of ‘functional’ rather than ‘material’ creation in Genesis 1 writes, “why should Israel be interested in material origins when no one else in the ancient world was?” But what if Israel, uniquely chosen by a unique God, was also granted a unique answer regarding material origins—after all, even to the current day there is no logically compelling non-biblical answer to “where did everything come from?” (Lawrence Krauss effectively redefines ‘nothing’ as ‘something’ in his 2012 *A Universe From Nothing*.) Beall points out that “most of the terms” in Genesis 1 “are quite normal (words for heaven, earth, water, darkness, light, day, evening, morning, birds, fish, sea, man, beasts, and so forth)” (p. 97) and universal, suggesting that the creation account was not merely intended for a specific ancient Near Eastern generation.

Walton contends that “the Bible, though written *for* us and all humanity, was not written *to* us” (p. 142, my emphasis). Although certain parts of Scripture are addressed to specific individuals or groups, the book of Genesis contains elements clearly identified in Scripture as addressed to people across the ages. For instance, in Galatians 3, Paul writes: “The promises were spoken to Abraham and *to* his seed . . . If *you* belong to Christ, then *you* are Abraham’s seed, and heirs according to the promise” (Galatians 3:16, 29, my emphasis). It is clear that the Abrahamic promises are spoken directly *to*, and not merely *for*, the heirs across time. In addition, Jesus, when asked about divorce, responds (to people who lived thousands of years after Moses): “What did Moses command *you*?” (Mark 10:3, my emphasis), citing Genesis 1 and 2 in his answer, and demonstrating that the creation account carries direct and diachronic covenantal consequences.

#### Authorial Intent

Related to the concept of ‘audience relevance’ is that of ‘authorial intent’.

Longman asserts that “inerrancy concerns what God *intends to teach* in a passage” (p. 104, my emphasis). But this is not correct—inerrancy regards not intent but rather the physical text itself. Similarly, Walton writes that “our biblical hermeneutics is designed to help us get at what the author intended to say” (p. 68), but this also does not seem to be quite correct. Hermeneutics strives to understand what a text means—not only what a text ‘intends’ to say but does not express (although there certainly are instances of figurative language in Scripture, in which denotation and connotation do not precisely overlap). The ‘locus of authority’ derives from the text itself and not from our speculations regarding the author’s unexpressed thoughts and intentions. The dangers of the ‘intent’ approach are exemplified by Longman’s subjective contention that “it is not necessary that Adam be a historical individual for the text to be without error in what it intends to teach” (p. 122). On the contrary, I think that it is absolutely necessary for Adam to be a historical individual in order for him to commit historical sin resulting in historical curses reversed by the historical life and death of a historical Saviour.

Turner states that “the reader should assume that the human authorial intent approximates, or serves as the starting point for, the divine intent” (p. 200), but this does not seem consistent with what the apostle Peter encourages: “Above all, you must understand that no *prophecy of Scripture came about by the prophet’s own interpretation*. For prophecy never had its origin in the will of man, but men spoke from God as they were carried along by the Holy Spirit [emphasis added]” 2 Peter 1:20–21; Moses identifies himself as a prophet in Deuteronomy 18:15). It is not the human writer’s own interpretation and ‘will’ which ultimately undergird the composition and meaning of the biblical text.

## Reflections

*Reading Genesis 1–2* provides us with a fascinating and comprehensive survey of contemporary views on the Genesis creation account. Not surprisingly, the non-literal interpretations of Genesis harmonize with modern scientific perspectives on origins. I would have liked to see more interaction (or indeed any interaction at all) with primary scientific literature such as the recent genetics studies which purportedly eliminate the possibility of the historical Adam. Moreover, I would have liked also to see, in the ‘non-literal’ chapters, interaction with New Testament texts which evidently depict Adam and the creation account to be historical realities. Throughout much of the book, Copernicu and Darwin serve as gatekeepers of acceptable inquiry, and I hope that the reader is inspired to conduct additional due diligence regarding the methodological, logical, and empirical underpinnings of the associated landmark theories. During my reading of the book I was continually amazed at Dr Beall’s “getting away with” his straightforward view of Genesis, given the current academic and intellectual climate—and I laud his courage, integrity, and insight. Overall, I highly recommend *Reading Genesis 1–2* to those interested in the question of origins and in the imponderable connections between premises and perceptions.

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# The emperors who had no clothes

I would like to comment on Dominic Statham's letter in the recent *J. Creation*.<sup>1</sup> The reason being that I think Milt Marcy has correctly captured something of Lyell's subterfuge, even if the quote given by Marcy is part of Lyell's historical sketch. I have recently written about Lyell, and his relationship with Darwin and others, and published this across several chapters in my book *Cracking the Darwin Code*. It is evident that Lyell's public statements have been at odds with his private thoughts and actions throughout much of his academic life (and others, such as Malcolm Bowden in *The Rise of the Evolutionary Fraud*, have pointed this out). It is true that Lyell appeared to reject progressive evolution in public statements prior to Darwin's publication of *Origins*,<sup>2</sup> but that is not the whole story. Lyell befriended Darwin when he returned from his *Beagle* voyage and, as Darwin commented, "Lyell entered in the *most* good natured manner, and almost without being asked, into my plans."<sup>3</sup> Lyell was one of only two people who knew of Darwin's secret notebooks that formed the basis of *Origins*, and encouraged him to write.

As well as supporting Darwin's work behind the scenes, Lyell was also secretly working to undermine the Anglican clergy, especially through involvement in geological science. Grinnell wonders why the Geological Society of London was so successful when other specialist societies failed for lack of interest, and notes that it was full of lawyers, doctors, and politicians. This interest may have been for the purpose of undermining the political establishment with its monarchical theory of government. The Tory Anglicans were influential in society and government and upheld the divinely appointed monarch and the scriptural foundation of law.

Attacking Scripture, Flood geology and the design argument weakened their position, as Grinnell, for instance, points out.<sup>4</sup>

Lyell's own letters reveal that he was working to 'free the sciences from Moses' through a secretive 20–30-year plan. This idea stems from Voltaire's methodology of a slow and silent attack against Christianity, which Lyell draws attention to. Lyell in fact followed Voltaire, perceiving the effective way that Christianity was undermined prior to revolution in France. On the 14 June 1830 Lyell wrote the following:

"I am sure you may get into Q.R. [Quarterly Review] what will free the science from Moses ... . If you don't triumph over them, but compliment the liberality and candour of the present age, the bishops and enlightened saints will join us in despising both the ancient and modern physico-theologians. It is just the time to strike, so rejoice that, sinner as you are, the Q.R. is open to you. If I have said more than some will like, yet I give you my word that full half of my history and comments was cut out, and even many facts ... it was anticipating twenty or thirty years of the march of honest feeling to declare it undisguisedly. I conceived the idea five or six years ago that if ever the mosaic geology could be set down without giving offense, it would be in an historic sketch."<sup>5</sup>

And when we turn to look at Darwin's letters we see that he was aware of, and was sympathetic to, Lyell's long-term plan. As Darwin admits, this was based upon Voltaire's maxim—that the best attack against Christianity was the slow and silent attack:

"... Lyell is most firmly convinced that he has shaken the faith in the Deluge far more efficiently by never having said a word against the Bible, than if he had acted otherwise ... . I have lately read Morley's Life of Voltaire and he insists strongly that direct attacks

on Christianity ... produce little permanent effect: real good seems only to follow the slow and silent attacks."<sup>6</sup>

"... yet it appears to me ... that direct arguments against Christianity and theism produce hardly any effects on the public, and freedom of thought is best provided by the gradual illumination of men's minds, which follow from the advance of science."<sup>7</sup>

When we look at the writing of Darwin and Lyell we may note that they admitted in private that they were promoting a cause through subterfuge. Dominic has of course previously commented along similar lines in a CMI article.<sup>8</sup> The cause was an attack upon the Anglican-Monarchical establishment with its commitment to the Mosaic basis of law, and to do that they sought to undermine Scripture and the doctrines of the church. They used a methodology first outlined by Voltaire as a slow and silent attack on Christianity.

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# Healthy genomes require recent creation

Alex Williams

Every organism alive today has had many generations of ancestors, and natural selection has acted upon ancestral variation and *de novo* mutations to adapt them to changing environments. As a result, fine examples of intelligent design like the bacterial flagellum and the peacock's tail can appear diminished by an apparent 'evolutionary continuum' when examined in the context of their many relatives and likely ancestral species. Darwinists naively claim these outcomes as random products of nature. To expose this groundless assumption I here take a different approach by looking at the decay of design. When viewed against the black backdrop of genome decay and species extinction, the designs of life emerge triumphant in what Darwinists have universally taken for granted—healthy survival. Healthy genomes, a concept underlying both genetics theory and medical practice, provide an irrefutable 'engineering timescale' argument for both intelligent design and recent origin. Genome decay projected forwards points to extinction in just thousands of years, and projected backwards it produces perfect copy fidelity in the very recent past. Darwinism is emphatically denied. Only Genesis-style fiat creation can explain it.

Many arguments and evidences for the intelligent design of life have been put forward, but they have gained little ground in the public consciousness. Counter-arguments from Darwinists continue to blind the eyes of the majority and the challenge remains for creationists to do better. To this end we need to look at the decay of design—and in particular at genome decay. This phenomenon is not only acknowledged by Darwinists (albeit sometimes unwittingly), it is indelibly written into genetics theory, and it forms the essential backdrop to understanding medical genetics. The consequences profoundly refute Darwinism, and they make Genesis-style recent creation undeniable.

## The neo-Darwinian genome

Darwinists believe that evolution on the grand scale is a fact:

*"As a well-established scientific fact, biological evolution still provokes heated debates all over the world about its compatibility with religious beliefs. ... both the scientific fact of evolution and the Darwinian theory are concerns of philosophy and theology ... [emphases added]."*<sup>1</sup>

Such unquestioned allegiance is almost universal today.

Darwin himself imagined that every slightly beneficial variation would be naturally selected, leading to improvement in the owner and its offspring, and that all such changes would work together in a continuously onward and upward direction:

*"As all the living forms of life are the lineal descendants of those which lived long before the Cambrian epoch, we may feel certain that the ordinary succession by generation has never once been broken, and*

*that no cataclysm has desolated the whole world. Hence we may look with some confidence to a secure future of great length. And as natural selection works solely by and for the good of each being, all corporeal and mental endowments will tend to progress towards perfection."*<sup>2</sup>

With the discovery of mutations and the new science of genetics in the early 20<sup>th</sup> century, Darwinism needed a new formulation. English statistician R.A. Fisher provided it in his 1930 book *The Genetical Theory of Natural Selection* in which he outlined what became known as the Modern Synthesis (what we usually call neo-Darwinian theory). Although his only data consisted of 500 deleterious mutations documented in the fruit fly *Drosophila*, he proposed that mutations of any kind had some chance of becoming beneficial to their hosts if they only produced small changes. This foundational assumption resulted in an exponential distribution of fitness effects (figure 1), which became the standard expectation in all subsequently genetics studies.<sup>3,4</sup>

When the structure of DNA and its implied information coding system was unveiled by Watson and Crick in 1953, Fisher's model was given a more concrete application. It now said, in effect, that any kind of mutation at any point on the DNA molecule had a finite chance of being beneficial if its magnitude of phenotypic change is small. Darwin's belief that every slightly beneficial variation would be naturally selected seemed to have been affirmed, and the neo-Darwinian genome became an indefinitely mutable entity. Fisher's theory now provided a clear foundation for the Darwinian belief that everything had evolved from something else.

If every form of life evolved from some other form of life, then every genome must, in principle at least, be

capable of being transformed into anything else. I shall here apply this principle to the human genome in relation to the great apes. If neo-Darwinian theory is correct, the human genome must be capable of having been transformed from a common ancestor with the chimpanzee and gorilla within the last 10 million years.<sup>6</sup>

### Genome in crisis

Orthodox Darwinists can only appeal to random changes and natural selection. But mutations that occur in genomic regions which affect conserved core structure are highly likely to kill their hosts. The only theory that has been put forward as a comprehensive solution to this challenge of why mutations do not destroy life is what molecular systems biologists Marc Kirschner and John Gerhart<sup>7,8</sup> called *facilitated variation theory*.<sup>9</sup> They noted that conserved core functions are modular, with ‘weak linkage’ between them. They likened the modules to Lego™ blocks that can be pulled apart and put together in different ways. The ‘weak linkage’ is provided by regulatory switching circuits that can be easily reorganized without damaging or changing the functional modules. As a result of this modular structure, natural variation would be built into the organism. Mutations and genetic rearrangements merely trigger into expression what is already present in potential. This creates a tremendous problem for evolution because it sets strict limits to natural variation and turns the ‘tree of life’ into a forest.<sup>10</sup> Thus, this theory hands creationists a ready-made explanation for within-kind variety.<sup>11</sup> It also provides built-in limits to natural variation, and allows very short timescales for diversification.<sup>12</sup>

### The medical genome

Neo-Darwinian theorists have always relied on a computational approach to mutations, but medical doctors have to deal with mutations in real life. Down syndrome was one of the first genetic disorders to be described in detail.<sup>13</sup> The cause—an extra copy of all or part of chromosome 21—thus constituted a pioneering result in medical genetics: a healthy human genome should only contain 23 homologous pairs of chromosomes, one complete set from the mother and one complete set from the father.

With the advent of DNA sequencing technology we are today discovering thousands of new genetic disorders every year.<sup>14</sup> Table 1 lists the numbers of genetic diseases (in rank order) published at the time of writing, totalling 156,932. Compare this to the tally for single nucleotide variations (SNVs, the simplest kind of mutation): 88 million.<sup>15</sup> An

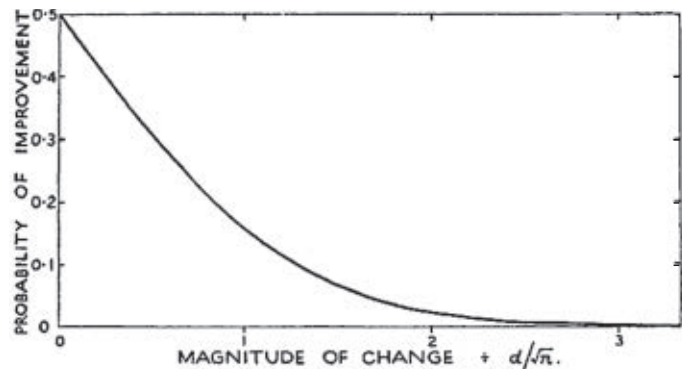


FIG. 3. The relation between the magnitude of an undirected change and the probability of improving adaptation, where the number of dimensions ( $n$ ) is large

Figure 1. R.A. Fisher's 1930 graph and caption for the magnitude of change produced by a mutation of any kind and the probability that it will improve the species' chances of survival.<sup>5</sup>

internet search on the topic of beneficial mutations in humans produced barely enough to count on one hand, and most of them were side effects of deleterious changes. The most promising was the claim that Tibetans had evolved an increased ability to absorb oxygen in the thin air of the Tibetan plateau, compared to Han Chinese. This conclusion was short-lived, however, since a subsequent study showed that the genetic signature had been inherited from ancestral Denisovans.<sup>16</sup>

According to the *1000 Genomes Project* the average number of SNVs per person today is 3.6 million.<sup>18</sup> A subsample of 179 healthy individuals found them to be carrying about 400 ‘disease associated’ mutations and 2 ‘disease

Table 1. List of disease-causing mutations from the Human Genome Mutation Database maintained by the Institute of Medical Genetics in Cardiff, Wales.<sup>17</sup> Every known kind of mutation appears in this list.

Type of Mutation	Number
Missense/nonsense SNVs	87,173
Small deletions	23,731
Splicing	14,302
Gross deletions	11,683
Small insertions	9,917
Regulatory	3,024
Gross insertions	2,797
Small indels	2,282
Complex rearrangements	1,567
Repeat variations	456
<b>Total disease-causing mutations</b>	<b>156,932</b>



causing' mutations.<sup>19</sup> Mutation databases are only recording 'deleterious' and 'functional' categories—there is no 'beneficial' category.<sup>20–22</sup>

Whole genome measurements of human mutation rates suggest a value in the region of 40 new SNVs per person per generation,<sup>23,24</sup> while a combination of methods suggests the rate is ~70.<sup>25</sup> Today we know that our genomes are 'full of functional elements'<sup>26</sup> and they are 'pervasively transcribed',<sup>27</sup> so it is likely that no mutation is truly neutral and all are likely to be at least slightly deleterious. A 'functional' mutation would thus be damaging, but not damaging enough to destroy function—although there is some controversy over the meaning of the word 'function'<sup>28</sup> in this context. A very telling argument on this point is that table 1 shows that *every known kind of mutation causes disease*. A recent review concluded:

"Finally, we examine models involving slightly advantageous mutations. We show that the distribution of the absolute strength of selection is well estimated if *mutations are assumed to be unconditionally deleterious* [emphasis added]."<sup>29</sup>

### Hereditary diseases

How do scientists decide when a genetic disorder is present? One indicator is heredity. Haemophilia—a defect in the blood-clotting mechanism that stops injuries from bleeding—figured prominently in the history of European royalty in the 19<sup>th</sup> and 20<sup>th</sup> centuries.<sup>30</sup> The mutation is recessive and occurs on the X chromosome. Females who carry one affected chromosome will not manifest the disease because the undamaged gene on the other X chromosome will produce the right protein for blood clotting. Males who inherit the damaged gene will normally manifest the disease because they have no undamaged gene to counteract it. However, there is also an anticoagulant system in the body that prevents clots from forming in inappropriate places, which would cause thrombosis. A male with a weakened anticoagulant mechanism will suffer less from inherited haemophilia than an otherwise normal male.<sup>31</sup> People with haemophilia B lack a protein called factor IX that is crucial for forming blood clots. Supplements of factor IX are currently used to treat it, but gene therapy is showing promise of a permanent cure.<sup>32</sup>

But more and more diseases today are turning out to have multiple genetic 'risk factors', sometimes hundreds of them. While many such diseases have a research history from study of families and twins, the latest methods included genome-wide association studies (GWAS). Disease complexes are identified by searching through the genomes of people with the disease compared with control subjects who do not have the disease symptoms. Examples of diseases with

multiple genetic risk factors include diabetes, heart disease, schizophrenia, multiple sclerosis, Alzheimer's, Parkinson's, ADHD, gout, celiac disease, lumbar disc disease, bipolar disorder, asthma, allergic rhinitis, atopic dermatitis, autoimmune disorders, Crohn's disease, stroke, autism, lupus, Paget's disease, and more.<sup>33</sup>

So how do doctors know what a healthy genome looks like? One way is to look at the chromosomes—a healthy genome contains an even number of matching chromosomes;<sup>34</sup> one complete set from the father, and one complete set from the mother. Any other combination is likely to cause disease. And where did the gene therapy researchers get their DNA with a functional factor IX gene? From the appropriate section of an *undamaged* X chromosome belonging to a person who did not suffer from haemophilia. Doctors recognize that mutations damage genes and cause disease.

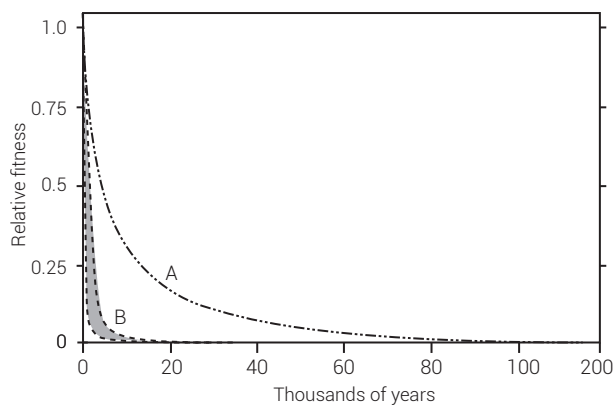
### The natural genome

Darwinists pride themselves on appealing only to natural causes, but cells have so many mechanisms to detect and remove mutations (DNA damage) that they clearly see changes to these systems as *un*-natural and damaging. DNA repair is such a burgeoning field of research that it now has its own research journal.<sup>35</sup> Cells also recognize when mutation damage is beyond repair—they invoke a 'suicide' option called *apoptosis* to dismantle the cell and recycle its components. Cells thus exercise natural self-selection and eliminate damage caused by too much mutation. This is entirely consistent with what medical genetics tells us.

Natural variation cannot be equated with mutation. Natural variation is primarily caused by that which is built into sexually reproducing organisms—the homologous recombination that takes place during meiosis.<sup>36</sup> Mutations add to variation, and sometimes can create new traits that selection can then focus on (e.g. sickle cell anaemia, because it provides some protection against malaria). Yet, since mutations are highly correlated with disease, they cannot be the sole, or even a major, source of variation.

### Genome decay

The fact that mutations lead to genome decay is now well established. Baer *et al.*<sup>37</sup> noted the widespread occurrence in multicellular eukaryotes of deleterious mutation rates greater than the threshold value of "one per generation" that would lead to "inexorable decay". Fisher should have realized it in 1930 when he gathered the available data on mutations and found that they were all deleterious. John Sanford's pioneering work,<sup>38</sup> which introduced the term 'genetic entropy', has now been supplemented with a number of other studies that confirm the devastating implications for



**Figure 2.** Human reproductive fitness decline due to genome decay. Curve A shows the rapid decline in fitness predicted by *Mendel's Accountant* using default human population parameters with today's mutation rate. The shaded region at B represents even more rapid fitness declines of 1% (upper curve) and 3% (lower curve) of today's values (per generation), as reluctantly admitted by leading genetics experts.

neo-Darwinian theory. The fundamental principle is easy to understand. Only lethal or strongly deleterious mutations can be removed from a population by natural selection. Slightly deleterious mutations are passed on. As they accumulate across generations, reproductive fitness declines and the species heads inevitably towards extinction. Numerous studies, using a variety of approaches, and all testifying to the same end, were published recently in *Biological Information: New perspectives*.<sup>39</sup> Most notably *Mendel's Accountant*, a comprehensive simulation of the fate of all new mutations in a population,<sup>40</sup> is proving to be an invaluable research tool. Even the digital evolution program *Avida* confirmed genome decay when biologically realistic data were used.<sup>41</sup>

The nearest that Darwinists have come to recognizing genetic entropy is in Muller's Ratchet—the inability of asexual species to remove deleterious mutations via meiotic recombination. But they believe the ratchet ‘clicks’ only when the least-mutant member of a population dies.<sup>42</sup> In reality the ratchet clicks multiple times every generation because a multitude of new mutations are added during each generation. Laurence Loewe's initiative was absurdly launched with the title “*Evolution@home*: Global computing quantifies evolution due to Muller's ratchet”.<sup>43</sup> But, as is clear from the scientific record, the ratchet leads to extinction, not evolution. Loewe found that genomic decay in human mitochondria presented an evolutionary paradox, and he had to acknowledge that nuclear DNA was equally threatened with extinction, so he appealed to “unconventional explanations for long-term persistence”.<sup>44</sup> He subsequently explored the problem in two asexual species,<sup>45,46</sup> then did a review of the field,<sup>47</sup> after which the subject disappeared from his CV.<sup>48</sup> His review included this observation: “one

can argue that extinctions are always caused by a lack of mutations that enable adaptation”.

To visualize the consequences of human genome decay, figure 2 shows the decline in reproductive fitness predicted by *Mendel's Accountant* using default human population parameters with the lower estimate of today's mutation rate (40 per person per generation). In addition there are two curves representing 1% and 3% fitness declines per generation which represent lower estimates of the impact of mutation load made (reluctantly) by leading geneticists.<sup>49,50</sup>

### Genome copying fidelity and reproductive fitness

Figure 2 shows that humans cannot possibly have evolved from a common ancestor with the great apes over millions of years. If we had been around for that long we would have mutated to extinction many times over. But it also raises serious questions about the state of our genomes if our species has existed for even several thousand years. Curve A in figure 2 shows a fitness decline to almost 40% after 6,000 years—is this realistic? According to a recent global survey,<sup>51</sup> primary infertility (inability to have a first child) affects about 2% of the world population, and secondary infertility (inability to have a second or further child) affects about 10%. Higher rates are found among older couples. Clearly the models represented in figure 2 are overestimating the impact of mutations on reproductive fitness.

How might we arrive at more realistic estimates? One way is to consider the amount of variation built into the human genome in the beginning. Carter has argued, and I agree, that since apparently healthy people today are carrying millions of SNVs then we should expect that our (perfect) original ancestors also carried millions of healthy variations (polymorphisms), originally put in place to produce phenotypic novelty, partially for future adaptation to changing environments.<sup>52</sup> If that is the case, the number of deleterious mutations accumulated since creation can be drastically reduced. Is there a way to estimate the number? Yes, there is—we can project genome copying fidelity backwards to explore the past.

Copy fidelity measures the success rate of genome copying rather than the error (mutation) rate. It is most easily understood when expressed in fraction or percentage terms. Starting from a perfect state, and with a fixed copy fidelity of 90%, a genome would contain more nonsense than information after just 7 generations ( $0.9^7 = 0.48$ ). It is obvious from these calculations that only very high initial copy fidelity could maintain a genome over many generations.

But does copy fidelity itself decay over time? Williams<sup>53</sup> recently explored the implications of a model with decaying copy fidelity for the origin of life. He demonstrated that life requires not only an extremely high standard of original

design and construction in its replication machinery, but also a high standard of ongoing maintenance and repair to sustain it over thousands of years. High genome copy fidelity requires the rapid and efficient detection and correction of copying errors and other DNA damage events. Many different systems are involved,<sup>54</sup> and new discoveries are continually being made.<sup>55</sup> Faithful replication of DNA support structures (e.g. histones) is also crucial to genome copy fidelity.<sup>56</sup> Here is a recent summary of the field of DNA repair:

“DNA repair is responsible for preserving the genome of all cellular organisms. [It also] controls mutation rates that generate genetic variation in response to environmental changes. These conflicting tasks are finely tuned ... [for] the difficult task of maintaining the proper balance of the entire repair system over a wide range of conditions ... . Moreover, DNA repair needs to be coordinated with DNA replication, transcription, and chromosome organization processes, which can in turn be regulated by damage responses. Although the main repair pathways [are known] we are still far from understanding the overall organization of DNA repair ... it is unclear how the different repair components cooperate to create functioning pathways, how the pathways coordinate and integrate with other cellular processes, and how environmental changes modulate the organization of the repair system.”<sup>57</sup>

In short, we don't yet know whether copy fidelity is decaying along with the rest of the genome or not. Nor do we know what form it would follow even if it were decaying. For

example, it might be collapsing exponentially, or it could be incrementally decreasing with each generation, or there may be a threshold (akin to the concept of mutational meltdown) where the fidelity slowly decays to a point beyond which it rapidly diminishes as the species approaches extinction.

But the following power function model allows us to explore copy fidelity in relation to the ‘healthy genome’ concept in a simplified manner. There are other possible scenarios, but they will all follow the same trajectory *in general*. Here is the basic equation:

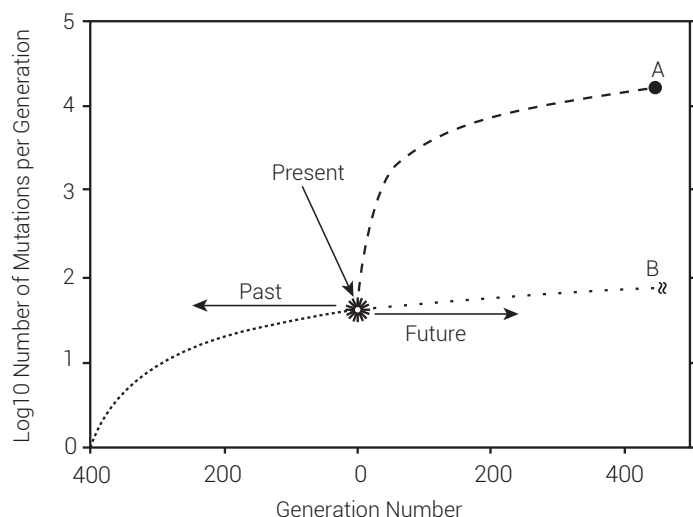
$$Q_t = (Q_0)^n \quad (1)$$

where  $Q_t$  is the copy fidelity at time  $t$  (in generations), and  $Q_0$  is the copy fidelity at some reference point  $n$  generations prior to time  $t$ . We don't know the exact contribution that copy errors make to our total mutation burden, but we can use the lower estimate from whole genome studies mentioned earlier (~40 per genome per generation) as a first approximation. We turn the mutation rate into a copy fidelity rate as follows: when projecting forwards,  $Q_0 = 1 - (40 \div 3,000,000,000) = 0.999999987$  (or 99.9999987%). The same number can then be used as the value of  $Q_t$  when projecting backwards into the past (figure 3).

Equation (1) can be solved forwards by iterating numerically through generations and accumulating mutations until the current average mutation burden of 3.6 million SNVs per person is reached. But numerical iteration of equations containing numbers close to 1 or 0 can rapidly accumulate

rounding errors, so the resulting value of  $n$  needs to be checked by substituting it into equation (1) and solving analytically for the number of mutations in the  $n^{\text{th}}$  generation. The result, using both methods, was  $n = 424$  generations (~8,480 years) (figure 3). Calculations were carried out using *Mathematica* v.9.0.1 (64-bit version), and 50-decimal-place precision was required to eliminate rounding errors.

Equation (1) can also be solved from some time in the past either iteratively by generation or by taking the  $n^{\text{th}}$  root of a value of  $Q_0$  which reproduces today's mutation rate. At exactly 400 generations into the past a value of  $Q_0$  equivalent to 1 error per 30 billion nucleotides per generation reproduced today's value of 40 copy errors per genome per generation. The error rate was so low at this earlier point that the genome would have been copied with 100% accuracy. Integrating the number of mutations produced in each generation over these 400 generations yielded a cumulative total of 8,020. This constitutes just 0.2% of today's mutation load of 3.6 million SNVs per person, so ‘other causes’



**Figure 3.** The behaviour of equation  $Q_t = (Q_0)^n$  starting from today's mutation rate (the asterisk symbol, which represents 40 mutations per genome per generation). Forward projection (dashed curve A) accumulates the current mutation load of 3.6 million per genome after 424 generations (~8,480 years). The dotted curve is the trajectory followed if the 'zero error' primordial copy fidelity is projected from the past through the present and into the future (curve B).



must have contributed the remaining 99.8%. This means that the previous forward projection of equation (1) gives a very large overestimate of the actual time required because copy errors could not have contributed more than 0.2% of today's total mutation burden.

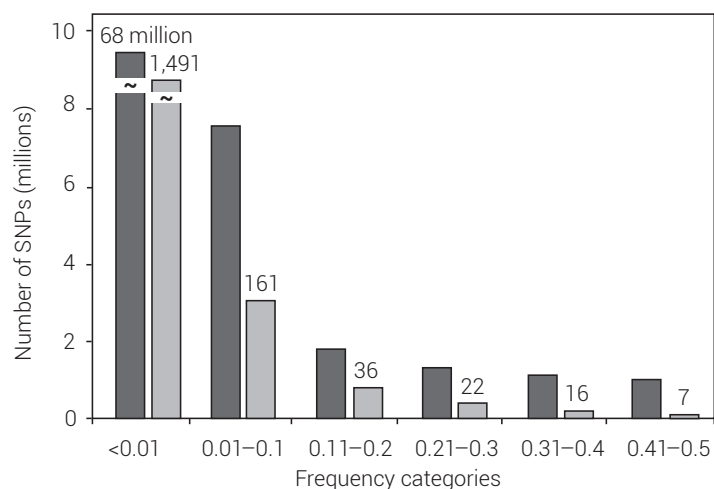
These considerations now give us a second way of projecting into the future. We can continue the primordial 'zero mutation rate' through today's mutation rate and then on into a future in which mutations accumulate at a much more slowly increasing rate. That is, copy fidelity remains much higher for much longer than in the earlier forward projection. In this case the model accumulated the present mutation burden in 8,485 generations (~170,000 years) from copy errors alone, which is again a very large overestimate because it ignores the major contribution from 'other sources' to today's SNV count.

If we follow Carter's argument we could say that the 99.8% of SNVs not attributable to copy error could be healthy polymorphisms that were present in our originating ancestors. Would this be more realistic? Perhaps, but we know that many kinds of events other than copy error can contribute damaging mutations to genomes, and we cannot know their precise history. Such events include ionising radiation from cosmic, solar, and local sources, toxins of many kinds in differing sources of food, air, and water, and reactive oxygen species that arise naturally in cellular metabolism and are not always promptly neutralized. Within the creationist model a hypothesized global period of accelerated nuclear decay is one potentially very large cause.<sup>58</sup>

Radiation therapists have long searched for ways to minimize radiation damage to healthy tissue. One enduring

mystery has been that patients vary enormously in their tolerance of radiation, with 80–90% of the variation being unexplained by standardized tests on tissue damage.<sup>59</sup> The recent availability of whole genome sequencing has shed some light. A study of reactions (in this case, erectile dysfunction) to radiation treatment for prostate cancer identified twelve SNVs that lie in or near genes involved in normal erectile function or other normal cellular functions, rather than [as expected] in mechanisms associated with DNA damage repair.<sup>60</sup> They showed that the risk of developing erectile dysfunction increased by 2.2 times for each extra SNV in these already mutation-damaged regions of their genomes.

Geneticists make an important distinction between SNVs shared widely in the population and those that are rare, usually only occurring in one or a few people or in localized populations. It is the latter group that contributes most to the wide variation in individual response to radiation therapy.<sup>60</sup> We can quantify this difference by referring to the dbSNP database.<sup>61</sup> Figure 4 gives the frequency distribution (dark grey bars) of all named and numbered SNVs identified in the '1000 Genomes Project' (81 million).<sup>62</sup> The vast majority of these, 68 million, are rare, with frequencies in the range 0.0001 to 0.01, and half of these, 34 million, are in the rarest category of  $\leq 0.0002$ . Among the common variants, 5.4 million fall in the range 0.01 to 0.5, and 13 million fall in the range 0.01 to 0.5. We can therefore reasonably accept Carter's conclusion: "I expect Adam had about 10 million or more heterozygous loci." Furthermore, only a total of 1,733 of these were identified as 'pathogenic' or 'likely pathogenic' (figure 4, light grey bars with numbers), which supports the idea that only a few thousand mutations have accumulated since creation.



**Figure 4.** Frequency distribution of total SNPs in the '1000 Genomes Project' data (dark bars, left hand scale in millions) and the few identified as 'pathogenic' or 'likely pathogenic' (light bars with numbers). In both cases the most frequent are the rare ones (far left columns).

We can now use the infertility data to shed light on the rate of genome decay. Secondary infertility is the value relevant to species survival—mothers must, on average, have more than two reproductively viable offspring to ward off species extinction. So we can use the current secondary infertility rate (10%) to calculate our species' reproductive fitness after 6,000 years at 90%. Assuming fertility factors are heritable in the same way that copy fidelity factors are heritable, and assuming a power function like equation (1), we can calculate reproductive fitness decline over time. In this case  $Q_t$  = fitness at time  $t$  (in generations), and  $Q_0$  = fitness in the first generation after the Fall.

The result of this calculation is  $Q_0 = 99.966\%$ . When converted to an infertility rate (for comparison with figure 3) it starts at zero and traces out a history that follows the shape of curve B, but with its origin at 300 generations

(6,000 years, assuming 20 years per generation). When projected into the future, infertility reaches 50% after 2,000 generations (40,000 years); beyond this point the population would rapidly decline to extinction.

We can also use *Mendel's Accountant* in a similar way to obtain a population-based estimate of the same history. A starting value of 5 new mutations per individual per generation, with the default human population values, is enough to reproduce today's infertility rate of 10% after 300 generations. During this period only 1,500 new mutations are accumulated. When projected into the future, infertility reaches 50% after about 12,000 generations (240,000 years), during which time about 60,000 mutations accumulate.

### Discussion and conclusions

These modelling exercises suggest that among the millions of SNVs in human genomes, only a few thousand are needed to explain the current decline in human fertility. When projected into the future it seems that only a few tens of thousands of similar mutations will be enough to drive us to extinction. Such conclusions are devastating for Darwinism.

Geneticists have long known that they face severe problems. James Crow addressed the National Academy of Sciences on fitness decline through mutation accumulation and concluded:

"I do regard mutation accumulation as a problem. It is something like the population bomb, but it has a much longer fuse. ... the characteristic time is some 50–100 generations, which cautions us against advocating any precipitate action. We can take time to learn more."<sup>63</sup>

But what is there to learn? Crow's timescale (and those in figures 2 and 3) is disastrous for Darwinism. Gene therapy is making headway<sup>64</sup> but at present is too risky to use on germ-line cells (eggs and sperm). And because we all carry a multitude of mutations and have identified hundreds of thousands of genetic diseases it is hard to know where to start in repairing a mutation-damaged genome.

The negative impact of mutations is built into genetics theory. The 'selection coefficient'—the central parameter that implements Darwin's theory—is defined as the fraction by which a mutant is *less fit* than the wild type. Nobel Prize-winning geneticist H.J. Muller defined 'mutation load' as "the overall *reduction* in mean fitness relative to the *mutation-free genotype* brought about by *recurrent deleterious mutation* [emphases added]".<sup>65</sup> Darwinists should stop being double-minded about their own subject matter and listen to what the medical profession is saying—mutations cause disease! Genomes are healthy only in so far as they are mutation-free.

How healthy are our genomes today? Adam could have carried millions of healthy variations in his genome, and most

of the millions we carry today could have been passed down to us unchanged. Deleterious mutations occurring after the Fall would seem to number only in the thousands. This makes the new mutation problem much more severe than previously expected. We are each carrying hundreds of mutations that have already degraded some of our organ systems to some degree, and the radiation therapy experiments show that every single new mutation doubles the risk of dysfunction to organ systems that are already damaged by mutations.

The models considered in this article all point to a primordial error-free 'healthy genome' just thousands of years into our past. There is no room anywhere—either in the experimental or theoretical data—for the Darwinian view of the human genome evolving 'upwards' over millions of years via mutation and natural selection. It simply does not exist. The inescapable conclusion is that humans must have been created with mutation-free 'healthy genomes' just a few thousand years ago, and their future is likewise limited to thousands, not millions, of years.

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# Nylon-eating bacteria—part 2: refuting Ohno's frame-shift theory

Royal Truman

Three decades ago Ohno proposed genes arose from simple oligomer repeats. He claimed that a 'T' insertion into gene PR.C consisting of multiple nt30 (CGACGCCGCT)<sub>3</sub> produced the ancestor of a new enzyme, E-II, which hydrolyzes Ald, a synthetic material of recent origin. However, our Blastp searches against the NCBI database found no proteins related to the product from PR.C. Using EMBOSS Needle it was not possible to align nt30 unambiguously to any of forty sliding windows 40 nt long from positions 1 through 79 in PR.C. These nt30 alignments were no better than thirty randomly generated sequences also 40 nt long having similar nucleotide distribution as PR.C. The optimal number of nt30 which align over the entire PR.C did not match as well as a simple chain of pure CG dinucleotides. Furthermore, the polypeptide chain derived from nt30 did not align with the PR.C's protein as well as a chain of pure arginines did. These and other tests reveal that the high C+G content of PR.C leads to statistical artefacts and no support for Ohno's frame-shift theory.

Ohno, a leading evolutionary theoretician, proposed several years ago that genes evolved from repetitive DNA sequences.<sup>1</sup> The probability of avoiding a *Stop* codon for  $n$  nucleotides (nt) is approximately  $(61/64)^{n/3}$  assuming each codon is equiprobable. For a small, 100-residue, polypeptide this results in a probability of  $(61/64)^{100} = 8.2 \times 10^{-3}$  and  $(61/64)^{300} = 5.6 \times 10^{-7}$  for an average size protein.

Ohno attempts to circumvent these low probabilities, pointing out that

"The situation is far more favorable with regard to repeats of base oligomers. Provided that the number of bases in the oligomeric unit is not a multiple of 3, three consecutive copies of it translated in three different reading frames constitutes the translation unit of such oligomeric repeats. Accordingly,  $(61/64)^{3n/3}$  simplified to  $(61/64)^n$ , the fraction of the repeats of  $n$ -base-long randomly generated base oligomers, shall have not one, but all three, open reading frames which equal the total length of repeats—e.g. 59.14% of the monodecameric repeats shall have all three reading frames open for indefinite length."<sup>2</sup>

Although simple repeat genes are not known to code for anything functional and would not be preserved by natural selection, suppose original genes consisted of multiple consecutive copies of 10 nucleotides. For three linked copies in a particular reading frame the probability of avoiding a *Stop* is about  $(61/64)^{3n/3} = (61/64)^{10} = 0.62$ . Ohno had to assume that for unknown reasons the alternative ORF did not generate mutations over millions of years, which would produce *Stop* codons.

Multiple identical sequences will eventually repeat, so linking monodecameric units which lack a *Stop* would ensure a long uninterrupted Open Reading Frame (ORF).

The length of the nucleotide sequence for each of the six reading frames, which would repeat endlessly, is easy to calculate.<sup>3</sup> It would therefore theoretically not be necessary to produce initial genes 100 to 1,000 nt long using random nucleotides in one step.

However, Ohno has avoided the low probability of generating average size genes of about 300 codons without a *Stop* codon at the price of introducing several other low probability requirements.

1. A particular 10 nt sequence is only one out of  $4^{10} = 1.048.576$  alternatives. A large number of alternatives would have to be somehow generated, linked together and tested by natural selection in an ancestral life form to determine whether that nt30-based gene worked.
2. Ohno assumed only the same kind of oligomers were linked together and in a suitable number.
3. A functional gene, based on linked 30nt, would have to actually work, without a *Stop* signal at all, and then this *Stop* would have to be added later at a suitable position. It is not clear whether Ohno assumes the genetic code already existed or a preceding form of life based on a different kind of information processing.
4. Single or double nt indels able to produce a *Stop* codon must be avoided during evolution.
5. It is exceedingly unlikely complex protein-based molecular machines could be built from such simple polypeptides. No examples are known of protein-coding genes composed of nothing but identical 10 nt repeats.
6. To be of any evolutionary consequence, the majority of genes would have to be shown to have arisen from shorter repetitive elements.

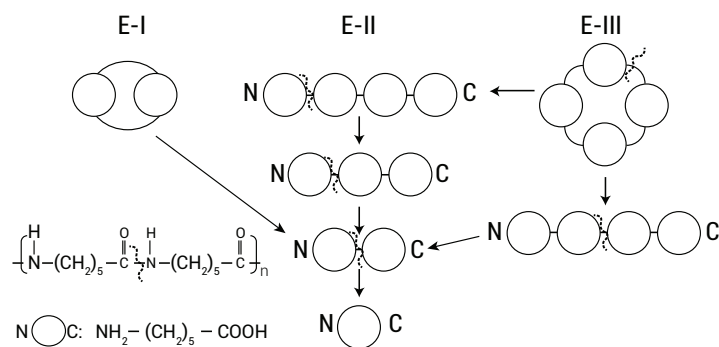


Figure 1. Degradation steps of nylon oligomers by enzymes E-I, E-II, and E-III.

### The origin of enzymes E-I, E-II, and E-III

Ohno applied his theory to explain the origin of some genes used by bacteria to degrade side products from the manufacture of nylon-6.<sup>2</sup> Since these synthetic substances did not exist during the lifetimes of the ancestors, the origin of the degrading enzymes has been used extensively by evolutionists as proof that most proteins could have arisen by chance, a line of reasoning disputed in Part 1 of this series.<sup>4</sup>

The enzymes required for the nylon-degrading pathway, E-I, E-II and E-III, catalyze the reactions shown in figure 1.

Genes for enzymes *E-I*, *E-II*, *E-E-II'* and *E-E-III* found in *Flavobacterium* sp. 172 were located on the same plasmid, pOAD2. *F-E-II* and *F-E-II'* are 88% identical<sup>5</sup> although *F-E-II'* displayed <1% activity towards 6-aminohexanoate dimer (see figure 1). Neither showed any reactivity toward natural amide compounds tested. The sequences of *F-E-II* and *F-E-III* were completely unrelated.

Another bacterial strain, *Pseudomonas* sp. NK87, also possessed enzymes, *P-E-I* and *P-E-II*, but the genes were located on different plasmids. Although *F-E-II* and *F-E-II'* were also very similar, the homology between the amino acid sequences of *F-E-II* and *P-E-II* was only 37%.<sup>6</sup> The authors claimed using evolutionary assumptions that the genes for *F-E-II* and *P-E-II* shared a common ancestor at least  $1.4 \times 10^8$  years ago.<sup>7</sup>

These observations show that enzymes able to hydrolyze amide bonds of synthetic materials can be sequentially similar or very different, and are sensitive to the chemical environment surrounding the amide bond being hydrolyzed, but say nothing about how they could have arisen since nylon began to be manufactured in the 1930s.

Yono also searched for long antisense strands lacking *Stop* codons, called Non Stop Frames (NSFs).<sup>8</sup> Remarkably, the antisense strands of the genes for *E-II*, *E-II'*, and *E-III* enzymes also contained long NSFs (*F-E-II*: 392 codons; *F-E-II'*: 392 codons; *F-E-III*: 394 codons; and *P-E-II*: 355 codons) and the regions coincide with those of the ORFs. The

antisense sequences of the aligned genes for *F-E-II*, *F-E-II'*, and *P-E-II* were even more different, in spite of supposedly having evolved from a common ancestral sequence.<sup>7</sup> They speculated that there is some special mechanism to protect these NSFs from mutations that generate *Stop* codons,<sup>8</sup> but we could not find any homologous proteins in the PIR and Swiss-Prot databases. Neither was Ohno able to identify homologous proteins for *F-E-II*, *F-E-II'*, *P-E-II*, and *F-E-III*.

### Putative origin of enzyme E-II

Understanding how the enzymes arose is fundamental to evaluating whether chance or pre-intended adaptability is more reasonable. Much of the debate has centred around Ohno's claim that one of the enzymes, *E-II*, arose from a chance point insertion, modifying the mRNA reading frame and leading to an entirely different protein.<sup>9</sup> This claim is often accepted as fact, and the significance of such a frame-shift argued<sup>10–12</sup> where the claim itself should have been examined more carefully, which we will now do. In Part 3 an alternative origin for *E-II* will be discussed, which specialists on the topic currently consider the better explanation. This reminds of so many cases in the evolutionary literature where interpretation of data became 'facts' or assumptions.<sup>13</sup>

Ohno's analysis had seemed compelling when published and interesting observations were brought to light. We decided to examine the data to judge whether a frame-shifted gene had arisen, considering that Ohno died in 2000 and thus can't defend his position.

### Ohno's Theory for origin of E-II

Enzyme *E-II* catalyzes the last reaction shown in figure 1 and variants have been isolated from different bacteria.<sup>2</sup> Ohno believed that the *E-II* isozyme (from gene *R-II<sub>A</sub>*), found on plasmid pOAD2 of *Flavobacterium* Sp. K172,<sup>14</sup> arose from a single T (Thymine) nucleotide insertion in a putative pre-existing gene he called PR.C ("Preexisted Coding sequence").<sup>2</sup> He observed that by removing a T from *E-II* a long stretch of nucleotides uninterrupted by *Stop* codons results, able to code for a 427-residue polypeptide.<sup>15,16</sup> Insertion of this T at nucleotide position 110 of PR.C (see figure 2) would have generated a *Stop* codon (TGA) in the original sequence and simultaneously produced a chain initiator codon (ATG) for the new 392 residue coding gene *R-II<sub>A</sub>*.

Ohno believed PR.C derived from several repetitive copies 10 nt long (CGACGCCGCT)<sub>3</sub> ('30nt'), which would generate identical strings every 30 nt,<sup>17,18</sup> i.e. every ten codons.

This sequence codes for Arg-Arg-Arg-Ser-Thr-Pro-Leu-Asp-Ala-Ala<sup>19</sup> (AA-10), a theory widely accepted.<sup>20</sup> Ohno was convinced the cyclic dimer and linear oligomer hydrolases also originated through frame-shift mutations, and wrote:

“I suggest that each of these unique genes for degradation of nylon by-products arose *de novo* independently from an alternative reading frame of the pre-existed, internally repetitious coding sequence. In particular, I suggest that the RS-IIA base sequence was originally a coding sequence for an arginine-rich polypeptide chain 427 or so residues long in its length and that the coding sequence for one of the two isozymic forms of 6-ALA LOH arose from its alternative open reading frame.”<sup>21</sup>

### Search in vain for the proposed PR.C sequence using Blastp

The theory assumes a copy of putative PR.C mutated to form E-II. If true, we should find similar sequences among extant organisms. We used Blastp software and the protein product from PR.C against the entire NCBI dataset but no candidate matches were found. We then limited the searches to 50 residue portions of PR.C.<sup>22</sup> Four of these portions found nothing remotely plausible, one matched poorly to a hypothetical protein, and the remaining three 50-aa sections of PR.C had poor overlap with sections of other proteins. To date no transcripts for PR.C have been reported.

### Repeat sequences offered as evidence PR.C existed (see Appendix 2<sup>23</sup>)

The existence of several short repeat polypeptide sequences in hypothetical gene PR.C was offered by Ohno as evidence for the repetitive nature of its ancestral gene (Appendix 1<sup>24</sup>).<sup>2</sup> We compared his repetitive patterns to

a chain of (AA-10)<sub>3</sub>; sequence 1 using the 1-letter abbreviations for amino acids for convenience, and confirmed that a double repeat of A-R-R-R in PR.C was present in a chain of (AA-10)<sub>3</sub>. Furthermore, double copies of tetrapeptides R-R-S-G and R-R-R-R matched at three out of four residues, and so did three copies of R-A-A-R. However, in other cases double repeats of tetrapeptides in PR.C have no reasonable region of overlap in (AA-10)<sub>3</sub>; for example, G-L-G-G, R-S-A-L, and R-A-A-A.

Ohno also drew attention to two similar decamers,<sup>2</sup> Dec1: R-A-D-R-R-G-A-H-R-S and Dec2: R-L-D-R-R-A-G-H-R-S, but visual inspection and using ClustalX shows insignificant overlap with a chain of linked AA-10, even using an unrealistic number of insertions or deletions: sequences 2 and 3. The repeats are scrambled all over PR.C, and Ohno did not discuss how these could have arisen from a (AA-10)<sub>n</sub> chain. Any mutational pathway would need to avoid creating *Stop* codons and produce functional proteins at every step. The PR.C gene and the resulting protein are *purely* hypothetical, and no similar sequences in other extant proteins were found by him or us.

### Does the beginning of PR.C match an nt30? (see Appendix 2)

If PR.C evolved from a chain of nt30s it should be easy to find the first one near the beginning of PR.C unambiguously, as discussed in Appendix 2. We used EMBOSS Needle to align nt30 against sliding windows 40 nt long for PR.C positions 1–79. The forty comparisons had 15 to 23 perfect nt alignments, with an average of 19.9 nt and standard deviation  $\sigma = 1.67$ . All forty required many indels. None of the alignments used any of the first four nt positions of PR.C (i.e. the algorithm had to treat this region as an insertion).

We compared the quality of nt30 alignments for these 40 sequences using EMBOSS Needle with thirty randomly

																		Start Codon																			
																		M			N			...		V			Stop								
																		34			35					425			426								
PRC.C.:	1			...		33													34			...		425			426			...							
	M					R													E					V			G										
	11	12	13			107	108	109	110	111	112	113			1284	1285	1286	1287	1288	1289																	
						C	G	A	T	G	A	A			G	T	A	G	G	C																	
	Start								Stop Codon										Stop																		

(Putative PR.C. If lacking T found in R-IIa would be have a huge ORF)

**Figure 2.** Gene R-II<sub>A</sub> was proposed to have arisen by a T nucleotide insertion in putative precursor gene PR.C, leading to a reading frame-shift. For the full sequence of R-IIA and PR.C see ref. 2.



(R-R-R-S-T-P-L-N-A-A) - (R-R-R-S-T-P-L-N-A-A) - (R-R-R-S-T-P-L-N-A-A) (1)

AA-10: R R R S T P L D A A R R R S T P L D A A (2)  
Dec1: - - R - - - - - A D R R G A H R S - -

AA-10: R R R S T P L D A A R R R S T P L D A A (3)  
Dec2: - - R - - - L D - - - R R A G - - H R S.

PR.C (5-44) CGA-GCCATGGGCTACATCGATCTCTCCGC-CCCCGTCGCG (4)  
nt30 CGACGCC----GC----TCGA---CGCCGCTCGACGCCGCT)

Random #27 CCGGCACCGAGCCTGCCGGCACCG-TCG-CGCCGC- (5)  
nt30 -CGACGCCG---CT--CGACGCCGCTCGACGCCGCT.

Random #11 CCACGCCGGGTGG--GCCGCTC--CTCCGGCT (6)  
nt30 CGACGCC-GCTCGACGCCGCTCGACGCC-GCT.

Random #15: CGGCGCCCGTTGGCGCCCGCCAGCT (7)  
nt30: CGACGCCGCTCGACGCCCGCC-GCT.

PR.C (2-41) CGCCGA-GCCATGGGCTACATCGATCTCTCCGCC-CCCGTCG----- (8)  
30nt ---CGACGCC----GC----TCGA-----CGCCGCTCGACGCCGCT

PR.C (18-57) ACATCGATCTCTCCGCCCCCGTCG-CGATGATCGTCAGCGG-- (9)  
30nt ----CGA---CGCCGC-----TCGACGCCGCTCGAC-GCCGCT.

PR.C\_AA RRGYTFGDTR ERTFHRPAPRQVS RSRGRGADTR (10)  
10\_AA (40) RRRSTPLDAA RR---RSTPLDAA RRRSTPLDAA.

PR.C\_AA RRAARRARDA APRSRAAARG DLHRRIPRAA (11)  
Rs RRRRRRRRRR RRRRRRRRRR RRRRRRRRRR.

generated sequences having the same proportion of A, C, G, T nucleotides as PR.C. For the random set an average of 18.3 nt aligned with  $\sigma = 2.20$ .

Remarkably, the best alignments of nt30 occurred with cases from the random sequences. For example, for both data sets a maximum of 23 nt alignments were found but for the randomly generated data fewer indels were necessary: sequences 4 and 5.

Furthermore, notice that alignment 5 has a six-nt continuous region of overlap, whereas the maximum in sequence 4 is only 4 nt.

We also observed that the biologically most plausible best agreement with nt30, taking number of indels and perfect alignments into account, was with one of the randomly generated sequences: sequence 6.

We even find a seven-nt continuous region of overlap in 6.

Statistical coincidences in sequence data can deceive. This 22/32 perfect overlap could easily have been interpreted as evolutionary homology but is pure statistical coincidence.

As another example of the risk of being misled by statistic artefacts, we could assume one of the other randomly generated sequences had undergone a single six-nt deletion during its evolution (a multiple of three, and thus it would not create a frame-shift): sequence 7.

The impression of homology is overwhelming (19/25 perfect alignment with an eight-nt region of perfect alignment). Who would have suspected the top sequence had been generated randomly?

## Conclusions from Appendix 2

There was no obvious location within the first 79 nt of PR.C for an initial 30nt sequence. As an example, the best alignment with 30nt for positions 2–41 and 18–57 are as follows: sequences 8 and 9.

Both align at 21 positions and have a comparable number of indels. For all the 40 sliding windows systematically examined, EMBOSS Needle was forced to insert many indels to produce the best alignment. In fact, throughout the entire PR.C sequences this was necessary to permit any semblance of a reasonable alignment.

The highly skewed distribution of nucleotides in 30nt and PR.C ( $C + G > 70\%$ ) is responsible for the large number of possible alignments, apparently good fits unavoidable for statistical reasons only. Introduction of indels produced multiple alternative alignments of comparable quality.

Using the measured average number of alignment positions and standard deviation, we cannot reject the null hypothesis  $H_0$  = ‘The best alignment of nt30 within positions 1–79 of PR.C is due to chance’.

The analysis so far shows that good alignments between nt30 and PR.C is due primarily to the non-random distribution of nucleotides. We will show below that randomly generated sequences will align even better by optimizing the proportion of GC dinucleotides.

## Observations from Appendix 3<sup>25</sup>

### Analysis using nucleotides

Since the entire PR.C sequence is supposed to have derived from a chain of dozens of nt30 with no *Stop* codon, several fairly intact nt30 should be easy to find. We aligned varying numbers of 30nt copies systematically against PR.C using the default settings for EMBOSS Needle (figure 3), looking for the best fit.<sup>26</sup> The best candidate for an ancestral

PR.C would have consisted of about forty 30nt copies. The optimal alignment had 53.3% nt identity and 30.6% gaps, but none of the forty regions could be interpreted as being highly conserved, far less a complete series of linked nt30.

The high content of nucleotides C and G in both sequences provides many opportunities for different alignments upon adding a few judicious indels. Therefore, we aligned the entire PR.C sequence with the optimal number of only GC doublets, found also by trial and error using EMBOSS Needle. The best overlap had 52.8% nt identity with 25.5% gaps.

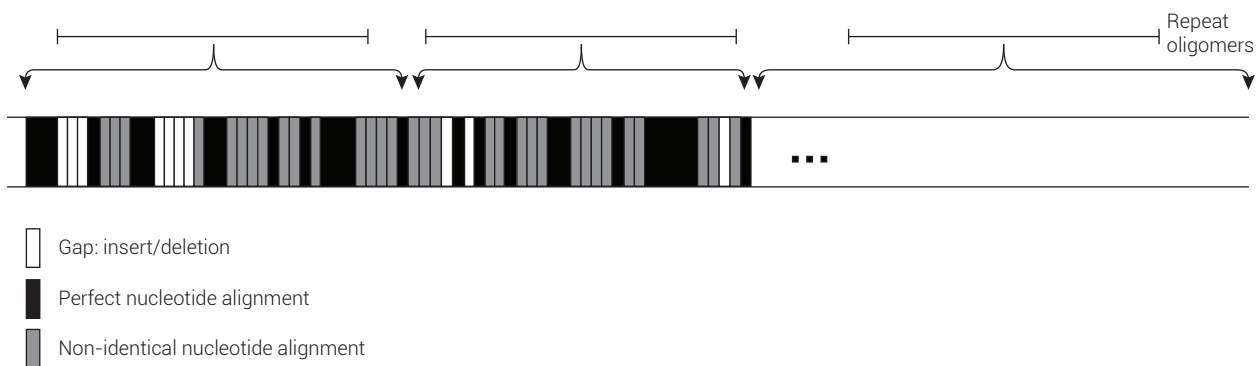
Recalling that CG pairs are often used for regulatory purposes, we examined the original PR.C sequence and found a predominance of CG vs GC pairs (202 vs 159). We showed that this is unlikely to be coincidence. Thirty randomly generated sequences of the same length as PR.C (1,287 nt) having the same proportion of A, C, G, T as PR.C were optimally aligned to a long CG chain. As expected, the average number of resulting CG pairs (156.0,  $\sigma = 8.24$ ) and GC pairs (158.9,  $\sigma = 9.25$ ) were almost identical for this random data set.

We also examined the alignment of a chain of pure CGC triplets of optimal length and determined this also aligned well with PR.C: 50.8% identity, 28.0% gaps.

In another experiment we examined whether other good candidates besides pure CG and CGC could be hypothesized in addition to Ohno’s nt30 sequence as an evolutionary starting point for PR.C. We reused some of the thirty randomly generated sequences mentioned above (i.e. having a similar proportion of nucleotides as PR.C), and replicated these to the length of the entire PR.C sequence. With little effort we already found one aligned example having 48.6% nt identity using 37.4% gaps with PR.C.

### Analysis using amino acids

Ohno claimed the ancestral polypeptide arose from a chain of multiple RRRSTPLDAA. We used the protein



**Figure 3.** The optimal number of identical 30nt repeats (top bars in black) were optimally aligned throughout the entire PR.C sequence using EMBOSS Needle. The best sequence alignments are shown under the 30nt repeats. See Appendix 2 for details.

version of EMBOSS Needle and found that 40 decapeptides produced the best alignment against the 429 residues coded for by PR.C (PR\_C\_AA). To help visualize the results, here are the first three aligned blocks: sequence 10.

The most likely first block was not near the origin of PR.C, but began at residue position 24. Over the entire PR\_C\_AA only 129 of the 429 residues aligned, after introducing 107 indels (23.1% gaps). Over half of the aligned decamers required one or more residue indels. Although seven different amino acids were present in the decamers (R,S,T,P,L,D, and A), only two accounted for most of the alignments: R = 68/129 and A = 24/129.

Further tests demonstrated that a chain of pure arginine (R) aligns considerably better than Ohno's proposed 10-AA chains. To help visualize the results, here is a 30-residue alignment near the beginning (residue position 63) of PR\_C\_AA: sequence 11.

Sequence 11 was not the best thirty AA aligned region. Although a chain of R and 10-AA both aligned at about 28% positions with PR\_C\_AA, the alignment with Rs only used about half as many indels (12.6% gaps). A single gap covering positions 1–32 of PR\_C\_AA represented most of the indels and would be far easier to justify than the multiple gaps all over the alignment found when using 10-AA.

### Conclusions from Appendix 3

Since the distribution of nucleotides in PR.C is significantly skewed (A = 15%; C = 37%; G = 33%; T = 15%) and thus 70.16% G + C<sup>27</sup>, we expected and demonstrated that good alignments can be found with randomly generated sequences if the nucleotide proportions are similar. The expected number of GC and CG pairs is about  $100 \times (0.7016/2)^2 = 12.3\%$  and for GC the content is as expected,  $100 \times (159/1286) = 12.4\%$ , but for CG it is significantly higher:  $100 \times (202/1286) = 15.7\%$ .

Not only does the 30nt oligomer proposed by Ohno have a similar distribution (A = 10%; C = 50%; G = 30%; T = 10) to PR.C, it benefitted from having a 60% to 40% proportion CG to GC pairs, which matches closely the proportion found in PR.C, unlike the randomly generated ones. In addition to the randomly generated blocks 30 nt long, there are countless others which would align better for every separate region within PR.C. Therefore, a repetitive structure for the ancestral PR.C has not been demonstrated since many alternative random sequences of the same length as PR.C would align better after taking the statistical factors into account.

Ohno did not offer any biological or chemical reason why the 10\_AA decamer should be reasonable. We demonstrated that better starting point candidates could be proposed which are unlikely to provide any value to an organism, such as a

pure CG chain. There is no doubt that many CG pairs are found in PR.C. It is known that these dinucleotides are often used to regulate genes in vertebrates, after cytosines in CpG dinucleotides have been methylated to form 5-methylcytosine CpG Islands.<sup>28</sup> Notice that the CpG section in the figure of this reference<sup>25</sup> resembles closely our results upon aligning a chain of CG against Pr.C.<sup>29</sup> Possibly a regulatory use for CpG remains to be discovered in prokaryotes.<sup>25</sup>

Pursuing the argument that reasonable-looking but biologically absurd alignments could be found, we demonstrated that a gene coding for pure arginine (R) aligns better with PR\_C\_AA than Ohno's decapeptide. This observation reflects the high C + G content of PR.C, since the codons for R are: (AGA, AGG, CGU, CGC, CGA, CGG). Thirty percent of 10-AA consists of R, which is very close to the proportion found in PR.C, so of course the EMBOSS could align both sequences after adding many indels.

### Discussion

In this paper we examined Ohno's frame-shift hypothesis, which claims ancestral genes evolved from short repetitive coding sequences. First of all, we demonstrated that the protein coded for by the hypothetical PR.C gene from which E-II supposedly evolved was not found in the NCBI database.

Statistical artefacts permitted us to offer other sequences which align better with PR.C and PR\_C\_AA than Ohno's 30nt or AA-10, although these are even more biologically absurd.

It was found that the major part (42%) of Ohno's hypothetical PC.R gene consisted of only two amino acids, Arg (28.3%) and Ala (13.6%), a peculiar protein at best.<sup>30</sup> Six codons code for Arg (AGA, AGG, CGA, CGT, CGC, CGG) of which 13/18 are C or G. For the four Ala codons (GCA, GCC, GCG, GCT), 10/12 are C or G. Since 70.2% of the sequence under study is C + G and not 50% as expected for an equiprobable nucleotide proportion, much higher proportions of Arg and Ala are to be expected merely by chance in the putative PR.C gene.

### Reasons for long ORF in PR.C

Note that the lower than expected number of *Stop* codons can be largely explained as coincidence. The three codons (TAA, TAG, TGA) consist of only 2/9 nucleotides C or G, and the start codon (ATG) is 1/3 C + G, and thus will be significantly underrepresented in a sequence of high C + G content. These factors contribute to longer theoretical ORFs being found in C + G-rich sequences.

Ohno calculated the probability of obtaining such long NSFs, taking the high G + C contents into account across all six reading frames for the four enzymes.<sup>31</sup> Assuming the



original gene possessed a 392 codon NSF, using evolutionary assumptions and the estimated time of divergence led to a probability of 0.007.<sup>32</sup> The authors speculated that some unknown mechanism must have been at play for tens of millions of years, which prevented the *Stop* codons from arising in an alternative reading frame, which then led to EII. However, a 0.7% probability is not prohibitive given the large number of organisms possessing high C + G gene contents.

Of course, this could more plausibly be interpreted as strong evidence that such genes have not been mutating for over a hundred million years. Note that the genes producing the enzymes which degrade synthetic substances were not essential for this purpose during the vast period of time, so accidental creation of *Stop* codons in the non-coding frame (the future EII) would not be selected against. Yomo recognizes the difficulty of somehow avoiding *Stop* codons in randomly mutating genes; for example, non-essential duplicate copies:

“For example, when the homology of the sequences between the duplicated gene and its original one with 392 codons becomes 50%, the probability of the duplicated gene still occurring is only  $6.8 \times 10^{-6}$ . Therefore, we conclude that preparing new NSFs and keeping the NSFs open are basic mechanisms for the occurrence of new enzymes.”<sup>33</sup>

For young earth creationists lack of a *Stop* codon might simply mean a few thousand years of mutations was not long enough to generate harmless *Stops* in alternative NSFs. Alternatively, it is possible that mutations able to produce a *Stop* codon in the other reading frame of EII’s ancestor would destroy a necessary pattern needed for alternative codes. This line of reasoning is problematic for an evolutionist, since it implies very little tolerance to random mutations, the source of evolutionary opportunity.

### Repetitive DNA sequences

We pointed out, based on the analysis presented in Appendix 2, that the evidence for a repetitive 30nt gene precursor is lacking, although some repetitive nt patterns may be present due to designed regulatory elements not related to protein coding.<sup>34</sup>

The chance of random frame-shifts leading to a properly expressed gene, coding for new enzymes like E-I, E-II and E-III, based on properly folded proteins, *which all happen to hydrolyze amides*, is infinitesimally small if by chance. The enzymes are structurally very different, and found on the same or different plasmids and even the bacterial chromosome. Subsequent to Ohno’s publications, biodegradation of nylon-6 was reported by Negoro for many other micro-organisms, such as those present in intrauterine

contraceptive devices *in vivo* and also biodegradation of nylon-6,6 by a lignin-degrading fungus.<sup>35</sup>

There has been no suggestion of frame-shifted genes nor repetitive structure for these new discoveries. In the case of the lignin-degrading fungus, the activity profile was identical to the reaction catalyzed by horseradish peroxidase, involving removing of a hydrogen radical from the methylene adjacent to the nitrogen. This mechanism is completely different than the breaking of the amide bond, key to the studies described above by Ohno. Degradation of synthetic materials used to manufacture nylon is apparently quite easy to catalyze and no single common ancestral gene needs to be postulated.

### Perspective

Highly adaptable micro-organisms able to cope in many environments and perform various ecological services is what the creation model expects.<sup>36</sup> Activation of cryptic information or multiuse DNA coding is certainly sensible if carefully *designed* in advance, and supports Borger’s Baranome Hypothesis (or preformation-hypothesis or front loaded hypothesis).<sup>37</sup>

Creation scientists have used the existence of proteins based on different reading frames as evidence for design, since this happening by chance defies credibility, especially in higher organisms like humans with long generation times.<sup>38,39</sup> However, the genes under discussion here are unlikely to have originated in this manner.<sup>40</sup>

In a recent rebuttal to evolutionary claims in CreationWiki we read, “The frame-shift mutation did not add onto the existing DNA rather it only scrambled what was there and because it is in an environment to adapt to, it worked!”<sup>41</sup> However, a frame-shift is not how this enzyme arose, and Ohno’s hypothesis should be confused with facts to be interpreted.

Other creation researchers are aware that the frame-shift theory, for which the evidence initially seemed compelling, is incorrect.<sup>42</sup> There is no reason information could not have been front-loaded,<sup>43</sup> able to be switched on instantly, *contra* the neo-Darwinian view of countless random and mostly non-productive mutations. However, Ohno’s incorrect proposal for the origin of nylon-digesting enzymes was accepted uncritically as fact, especially his claim that a repetitive oligomer was the evolutionary starting point. This was spun into a dogmatic story which supposedly proved the overreaching claims by evolutionist theory such as Thwaite’s three-decades-old statement that

“... creationists, and others who should know better are dead wrong about the near-zero probability of new enzyme formation”.<sup>44</sup>

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- The chance of a fully random DNA sequence being able to code for a protein able to fold properly (and/or perform a biological service) is negligibly small. But the Creator could select coding sequences for the primary function which when read in another reading frame would also work. The sequences would have been very carefully selected and virtually impossible to recognize using existing statistical tests for randomness. However, if far more frame-shifted genes were found to produce functional proteins than random sequences with the same nucleotide proportion, that could be interpreted as evidence for informational front-loading.
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# Difficulties with plate tectonics—Pacific Ocean bottom features

Michael J. Oard

Plate tectonics assumes that crustal plates have moved thousands of kilometres. Examples include the Pacific Ocean bottom. Some biblical creationists accept the movement, though not the slow pace of events. Others do not accept major plate movement. Evidence for a lack of large-scale tectonic plate movement is presented from features on the bottom of the Pacific Ocean. If the Pacific Plate has moved thousands of kilometres northwest with respect to the North American Plate, as uniformitarian scientists believe, Monterey Canyon and Fan would have become offset by around 150 km, but little relative movement is indicated. Moreover, the Zodiac Fan that originated from western Alaska on the Pacific Plate has moved little relative to the North American Plate and the eastern Aleutian Trench did not exist during fan formation. Finally, the Meiji sediment tongue in the northwest part of the Pacific Plate lacks a sediment source at its origin presumed by plate tectonics in the middle of the Pacific Ocean. It is hoped that this paper will advance the current discussion toward a fuller and more unified view of Flood geology.

The large-scale picture of biology and sedimentary rocks with their contained fossils overwhelmingly favours creation and the Flood, as described in the early chapters of Genesis. In regard to sedimentary rocks, the fact that some formations can be traced thousands of kilometres with little evidence of erosion between, and within, the sedimentary rock layers is powerful evidence for rapid Flood deposition.<sup>1</sup> These observations are contrary to uniformitarian ideals.

Nevertheless, building a Flood model is a difficult task, and several have been proposed. One of these is the catastrophic plate tectonics (CPT) model, which has many issues to work out.<sup>2–5</sup> Based on geodetic measurements and tomographic data, it is claimed that plate tectonics (PT) is still occurring today.<sup>6,7</sup>

Regardless, the real evidence for CPT and PT should be evidence that *plates have moved thousands of kilometres* in the past. (For the purpose of clarity, plates are defined as areas of the Earth's lithosphere that are separated by major faults and/or volcanism.) In my view this is the *definitive* test regarding the explanatory efficacy of CPT and PT. The issue of whether there is present movement of plates or portions of plates is secondary and can be interpreted differently. For example, the GPS data that Baumgardner claims support CPT<sup>8</sup> can also be explained by residual horizontal and vertical motions after the Flood.<sup>9</sup>

Evidence for the claimed thousands of kilometres of plate movement in the past comes from issues such as the magnetic anomalies (or 'stripes', as they are nicknamed) in the ocean-bottom rocks and the 'fit' of the continents across the Atlantic Ocean. However, these magnetic anomalies are *not* reversed and normal ocean crust, as believed for many years, but are less than 1% changes in magnetic *intensity*.<sup>10</sup>

Drilling into the basalt on the ocean bottom has revealed a hodge-podge of normal and reversed directions, which does not accord with systematic reversed and normal magnetic directions in lava that are parallel to the mid-ocean ridges.<sup>11</sup> Thus the anomalies mainly originate deeper than the basalt layer. They likely derive from the gabbro of the lower ocean crust and the peridotite of the upper mantle. Moreover, since the magnetic anomalies are intensity variations, the depth of magnetization could imply that the stripes are in fact systematic changes in the magnetic properties of the lower crust and/or upper mantle, such as magnetic susceptibility (a measure of the degree to which a rock can be magnetized).

The Pacific Plate is supposedly moving at a rate of about 6 cm/year in a northwest direction with respect to the North American Plate, which actually starts in Central America and wraps itself around the northern Pacific Plate through Alaska and northeast Asia to about Japan. This paper will show that the Pacific Plate has moved little with respect to the North American Plate.

## Monterey Submarine Canyon and Fan show little movement on San Gregorio Fault

The San Andreas Fault, considered a long transform fault, passes to the east of Monterey Bay in west-central California, USA. However, it is actually a wide fault *zone* with several different smaller faults from the San Gregorio fault offshore of Monterey Bay in the west to western Nevada in the east (figure 1). The fault zone in western Nevada is called the Walker Lane, where 25% of the relative plate motion between the North American and Pacific



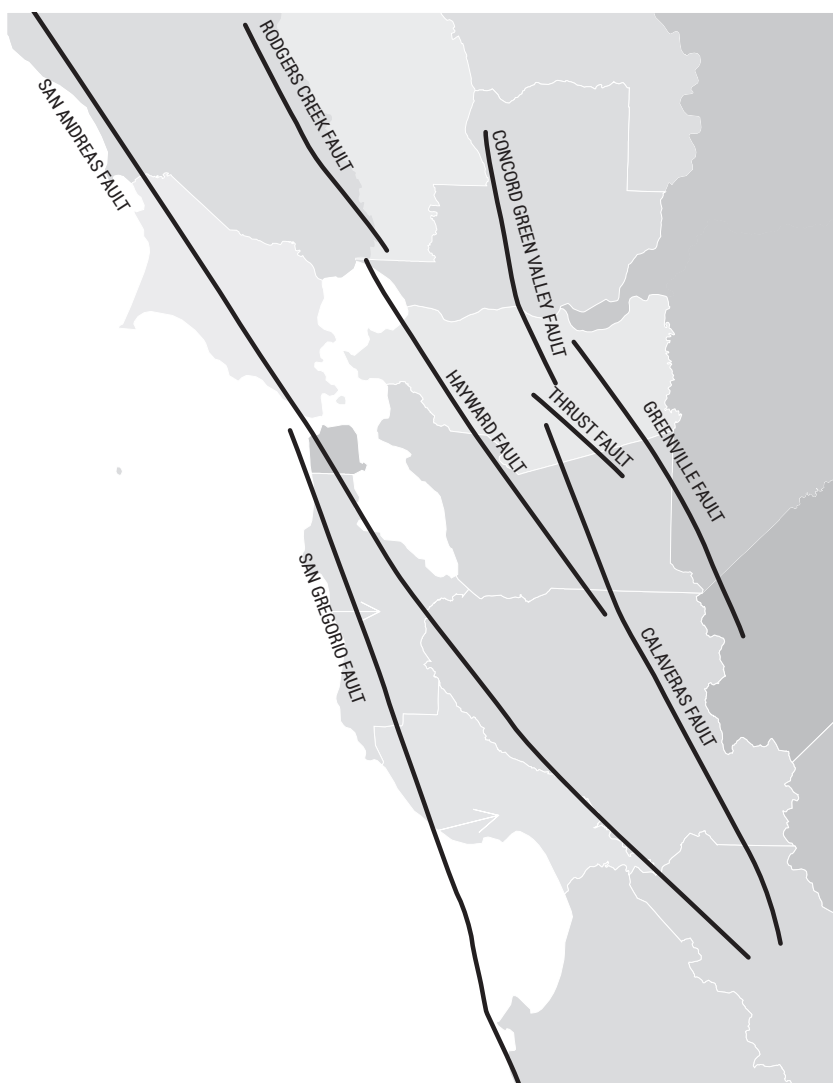
Plates presently takes place.<sup>12</sup> Based on geodetic data, the current relative motion between the Pacific Plate, moving northwest, and the North American Plate, moving west, is estimated to be about 6.5 cm/yr.

The Monterey Submarine Canyon extends westward from Monterey Bay. It is 95 km long, and, like so many other submarine canyons, it extends westward on top of a large submarine fan, called the Monterey Fan (figure 2).<sup>13</sup> If the westward-extending fan valley entrenched on the Monterey submarine fan is included, the total length of the canyon is 470 km.<sup>14</sup> Its maximum wall height is 1,700 m, and its maximum rim-to-rim width is 12 km. It is similar in depth and width to the Grand Canyon. The Monterey Fan covers over 100,000 km<sup>2</sup> and has an average thickness of 1.5 km with an estimated volume of 150,000 km<sup>3</sup>. The Monterey Submarine Canyon and Fan would have been formed late in the Flood by channelized Flood currents during the Dispersive Phase of the Flood.<sup>15,16</sup>

The San Gregorio fault, the boundary between the Pacific Plate, to the west, and the western San Andreas Fault zone, passes through Monterey Submarine Canyon at about 1,800 m below sea level.<sup>17</sup> The fault is delineated by earthquake epicenters and small topographical features within Monterey Canyon. The lower part of the canyon and the submarine fan is on the Pacific Plate. Based on geodetic measurements on land to the north, the San Gregorio Fault is presently moving at about 6 mm/yr.<sup>18</sup> At that rate, it would have slipped 6 km in a million years and 180 km in 30 Ma, according to the uniformitarian timescale. It has also been assumed that the west side of the San Gregorio Fault has moved northwest 70 to 150 km with respect to the east side since the mid Miocene Epoch within the uniformitarian timescale, but some think the movement is less.<sup>17,19</sup> Dickenson recently reanalyzed the fault movement and, based on geology, he came up with a fault movement of 156 km since it first developed in the late Miocene.<sup>20</sup>

However, the geomorphology of the canyon suggests there has been very little contrastive movement between the upper canyon and the

lower canyon and fan. Slip appears to have been much less along the San Gregorio Fault, especially for the past few million years within the evolutionary timescale.<sup>21</sup> In fact, there is little evidence of significant fault movement from sonar images and topographical relief on the upper continental slope and shelf north of the canyon.<sup>17,22</sup> The linear Carmel Canyon, which runs into Monterey Canyon from the south, and the displacement in Monterey Canyon where the fault crosses the canyon are thought to be manifestations of the fault. It appears that the displacement is only about 3 km, if really caused by fault movement. So, though it seems likely that the fault runs through Monterey Canyon, the geomorphology suggests that there has been *little horizontal movement* on the fault, contrary to the extensive movement predicted by the plate tectonics model.<sup>23</sup>



**Figure 1.** San Andreas Fault zone in Central California. Note that the San Gregorio Fault passes through the western Monterey Bay (redrawn by Mrs Melanie Richard from a USGS map).

Thus, it is likely that the Monterey Fan is a depositional product derived from sediments eroded around, and to the east of, Monterey Canyon during the formation of the canyon late in the Flood and afterwards.<sup>16,24</sup> This would imply that there was not 150 km of horizontal movement between the Pacific Plate and the San Andreas Fault zone, and probably the North American Plate.

Advocates of CPT could claim either that the San Gregorio Fault is a very new fault (a post-Flood fault) or its movement has been much less than uniformitarian scientists claim. But in so doing, they would be going against the ‘calculated’ claims of movement by the uniformitarian scientists.

### The Zodiac Fan from western Alaska

Granted that there has been little movement of the lower Monterey Submarine Canyon and Fan with respect to the upper part of the canyon, there are other bottom features on the Pacific Plate that indicate even more of a discrepancy. In the northern North Pacific, the huge Zodiac Fan lies just to the south of the Aleutian Trench and west of the Patton-Murray Seamount Chain in the northwestern Gulf of Alaska, and extends down to about 44°N at 160°W (figure 3).<sup>25</sup> The fan is estimated to cover an area greater than 1,000,000 km<sup>2</sup> with a volume of 280,000 km<sup>3</sup>, giving it an average thickness of 280 m.<sup>25</sup> The most striking feature of the fan is the well-developed channels network that trends north to northeast with levee overbank deposits, indicating that the fan was built up from a south

to southwest flow of sediments. Furthermore, the sediments are terrigenous, meaning they came from a continental land mass. Based on fossils, the fan is dated from the late Eocene to early Oligocene, around 24 to 40 Ma ago within the uniformitarian timescale. The source of the sediments gives indications of originating from the Alaskan Peninsula and western Alaska.

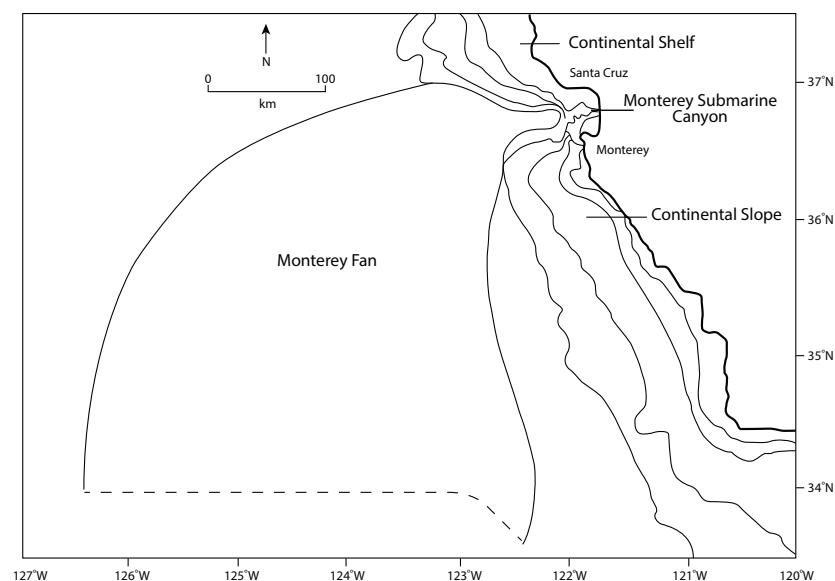
It is interesting that before the Alaska Range uplifted, the sedimentary rocks of the late- to mid-Cenozoic Usibelli Group were deposited by paleocurrents flowing toward the *south to southwest*.<sup>26,27</sup> The Usibelli is about 600 m thick, widespread, and consists of pebbly sandstone interbedded with coal and mudstone. Paleocurrent directions can be determined, especially from cross-beds in sandstones and the imbrication of oblong rocks in the gravel. The continuation of the paleocurrents during the denudation of Alaska in the Recessive Stage of the Flood would have helped build the Zodiac Fan.

The Zodiac Fan presents a major problem for plate tectonics. The Pacific Plate was supposedly moving northwestward during the Cenozoic and so the fan would have been in the middle of the Pacific Ocean, 1,500 to 3,000 km away, and far from any continental landmass during most of the Cenozoic!<sup>25</sup> If this were the case, where would the fan sediments have originated? The most straightforward interpretation of the data is that the fan was caused by massive erosion of Alaska during the Recessional Stage of the Flood, in which case it makes sense that there has been *little or no movement* of the Pacific Plate with regard to Alaska, which is on the North American plate.<sup>28</sup>

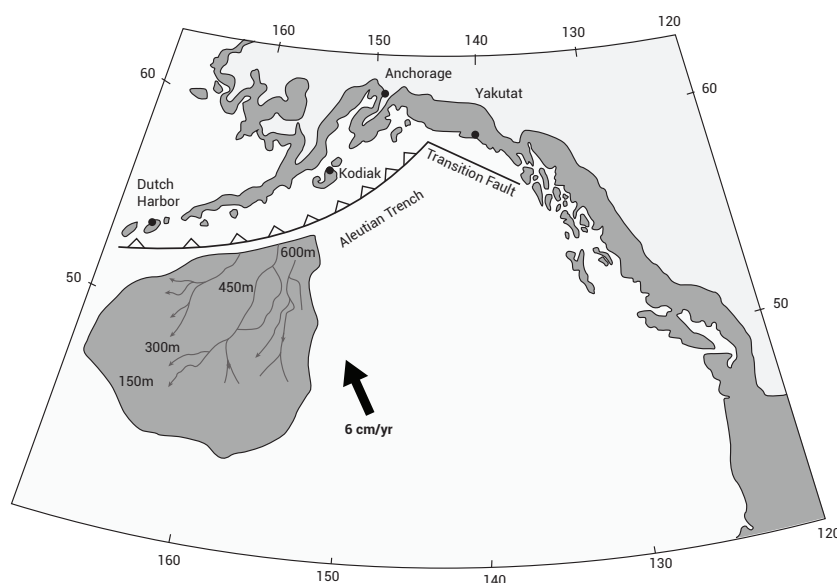
Moreover, the sediments had to cross the location of the Aleutian Trench, which implies that the trench was either non-existent or filled up:

“The sedimentary record from the Aleutian Abyssal Plain has important implications for plate tectonics in this area. If, as seems likely, the turbidite source was from Alaska to the north and northeast, then either no trench, or a filled trench, must have separated Alaska from the plain from middle Eocene to middle Oligocene times.”<sup>29</sup>

Since the eastern Aleutian Trench is not totally filled today, it is much more likely that the Aleutian Trench is a new feature formed after the Zodiac Fan, and therefore a late Flood structure formed by differential vertical tectonics.



**Figure 2.** The Monterey Submarine Fan offshore from Monterey Canyon (redrawn from Fildani and Normark, 2004<sup>13</sup>, by Mrs Melanie Richard).



**Figure 3.** The Zodiac Fan, south to southwest of Alaska, south of the Aleutian Trench, which has features indicating the huge fan sediments originated in Alaska (redrawn from Stevenson *et al.*, 1983,<sup>25</sup> by Mrs Melanie Richard). However, if the Pacific Plate moved northwest, the fan would have been in the middle of the northeast Pacific in the early to mid Cenozoic.

There have been a number of unlikely PT explanations for the anomaly of the Zodiac Fan. In 1986, Byrne proposed that, while the Zodiac Fan always collected sediments from Alaska, it was once much larger, and the northern portion subducted under the Aleutian Island arc.<sup>30</sup> This would mean the fan was several hundreds of kilometers larger in its north-south extent. But what about its extent up to 3,000 km to the southeast during the early Cenozoic?

In 1987, Harbert proposed a solution to the problem, positing that the source of the terrigenous sediments was the northwest United States,<sup>31</sup> although the fan was far from western North America in the early Cenozoic and has current directional indicators from the north. He states that the fan stopped collecting sediments when seamounts blocked the path of the sediments from the northwest United States.

Two years later, Pickering *et al.* proposed a different solution to the Zodiac Fan paradox. They assumed a weakly active trench due to discontinuous plate motion from the beginning of fan deposition up until the middle Oligocene, which allowed erosional sediments from Alaska to pass over the trench.<sup>29</sup> Then the trench became more active until the Pliocene to isolate the source from the fan. However, this still does not explain how the Zodiac Fan was deposited up to 3,000 km away toward the southeast, far from any land mass.

An advocate of CPT has offered an answer to this dilemma:

“This fan was formed almost certainly during

the early runoff stage of the Flood when the plate was located further to the east, adjacent to the Alaskan coast, and east of the eastern end of the Alaska trench.”<sup>32</sup>

However, in light of the material presented above, this explanation seems weak. The problem is that though both models assume that the fan formed during the early runoff stage of the Flood, its location to the east and not to the southeast, according to the northwest motion of the Pacific plate extrapolated backwards, is *ad hoc* and contrary to PT doctrine. Moreover, there is another large fan in the northeast Pacific Ocean called the Surveyor Fan.<sup>33</sup> GPS data shows the Pacific plate moving northwest, and the explanation for the Emperor/Hawaiian Islands as a hotspot trace depends upon this northwest movement. There is a glaring problem with the origin of

the Monterey Fan if the Pacific Plate moved thousands of kilometres west during the late Flood as required by CPT.

The straightforward interpretation of the Zodiac Fan is that it represents sediments deposited during the early Recessive Stage runoff from western Alaska, and that the Aleutian Trench did not exist at the time and, hence, is a young feature formed late in the Flood. This fits well with the differential vertical tectonics that drained the floodwater when the continents rose and the ocean basins sank.<sup>24,34,35</sup> The GPS data showing relative movement now would then be residual motion left over from Flood tectonics.

### The Meiji sediment tongue

Another perplexing ocean-bottom feature of the Pacific Plate for PT advocates is the Meiji sediment tongue, also called the Meiji Drift, in the northwest North Pacific Ocean. This is a deposit of sediments between the western Aleutian volcanic arc and trench and the Emperor Seamount Chain. The Meiji sediment tongue is greater than 1,500 km long, 300 km wide, and up to 2,000 m thick (figure 4).<sup>36,37</sup> The sediment tongue is thickest with a narrow width in the northwest and thins vertically with the width increasing toward the southeast, as expected if deposition was from the west or north, possibly through the 4,000-m-deep Kamchatka Strait. The Meiji sediment tongue has been accumulating sediment from southeastward-moving currents since the early Oligocene, 34 Ma in the

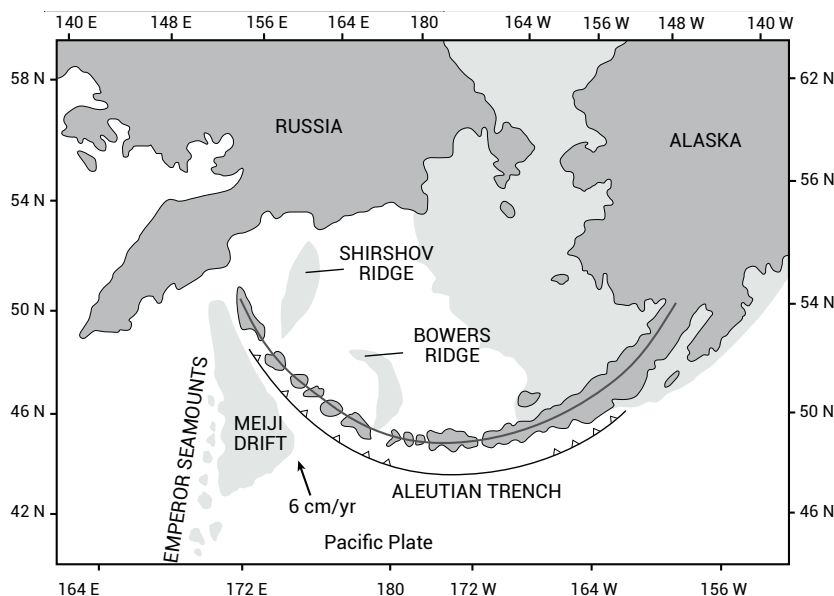


uniformitarian timescale.<sup>36</sup> The origin of all this sediment is a mystery within PT.

According to PT, the Pacific Plate has been moving northwest since the early Oligocene about 34 Ma ago. It is supposedly moving at about 6 cm/yr at present in relation to the northwest North American Plate of northeast Asia, which is west and north of the Meiji sediment tongue. At that rate the plate would have moved about 2,000 km. Therefore, the Meiji sediment tongue would have been greatly deformed and folded up against the Kamchatka continental margin. It seems unlikely that it has travelled anywhere near that far on the Pacific Plate because there would be no source for the fan sediments in the middle of the Pacific Ocean, 2,000 km to the southeast. The shape of the fan indicates that it has been collecting sediments right where it is since the early Oligocene. The straightforward interpretation is that there has been *very little movement of the Pacific Plate* northwest with respect to the North American Plate, contrary to the PT paradigm:

“A powerful argument can therefore be made that both the lower Tertiary turbidites of the Gulf of Alaska [the Zodiac Fan] and the finer grained Neogene terrigenous deposits of the Meiji sediment tongue are *near* their source terranes. Accordingly, the two sedimentary bodies represent formidable geologic evidence that, since early Eocene time (approximately the past 50 m.y.), the total displacement of Pacific lithosphere relative to that of the American plate has not been great [emphasis added].”<sup>38</sup>

The negligible movement of the Pacific Plate deduced from both the Zodiac Fan and the Meiji sediment tongue weigh heavily against the significant and rapid movement deduced from the Hawaiian Islands/Emperor Seamount Chain. (Interestingly, volcanism also occurred at 24 to 42 Ma ago in the far northern Emperor Seamount Chain, which is much younger than the dates of construction of the seamounts, according to the hot spot track hypothesis. This raises serious suspicions that the nice linear series of age dates from northwest to southeast in this hot spot track were singled out because they matched the idea of the Pacific Plate moving northwest over a hot spot rather than any pattern evident in the whole dataset.)



**Figure 4.** The Meiji sediment tongue in the northwest Pacific, showing evidence of having accumulated in its exact position, with little or no movement of the Pacific Plate relative to the North American Plate (drawn by Mrs Melanie Richard).

Like the Zodiac Fan, the Meiji sediment tongue collected sediments from Flood runoff during the early Recessive Stage of the Flood, with little horizontal plate movement.

## Discussion and conclusion

Creationists have long puzzled over the meaning of plate tectonics and, in particular, catastrophic plate tectonics within a Flood model. Many geological and geophysical problems have developed since the advent of the paradigm in 1960s that have not been resolved by PT and CPT. Advocates of CPT need to do the research that advances their model, but little has been accomplished over the past 30 years or so.

One problem is that there is evidence from Pacific Ocean bottom features that the Pacific Plate has moved little with regard to the North American Plate, which wraps around to the north of the Pacific Plate. The lower Monterey Submarine Canyon and Fan should have moved 150 km or so northwest in relation to the San Andreas Fault zone. The lack of significant horizontal movement of the Zodiac Fan and Meiji sediment tongue shows little horizontal movement between the Pacific Plate, one of the fastest-moving plates, and the North American Plate. There should have been thousands of kilometres of relative movement during the deposition of these features. This lack of significant lateral movement indicates that PT and CPT did not occur.

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# Improbable singularities—evolution is riddled with them

Alex Williams

Evolutionists claim their story of origins is based upon science only. This is not true. The evolution story (including its cosmic origins) consists of a long series of unique one-off events that are best described as singularities. Science can only deal with repeatable events, so singularities are normally beyond its reach. However, when evolutionary events are claimed to be naturalistic, repeatable, and subject to chance, then we can use probability theory to calculate the likelihood that they only happen once. The conclusion is that a long series of singularities is indistinguishable from a long series of miracles. As it turns out, all stories of origin consist of a series of singularities, so all of them are beyond the reach of scientific analysis. However, the causes and consequences of origin stories are open to scientific enquiry. The big events in the evolution story all lack credible causes. The biblical story does have a credible cause—Almighty God—and its consequences have abundant peer-reviewed supporting evidences in creationist literature. Regardless of evidence, however, the singularity problem is a reminder that origin stories are not built primarily upon science, but on history (notably the imagined eons of time in evolution), philosophy, and a resulting worldview.

On 29 March 1863, four years after publishing the first edition of his *Origin of Species*, Charles Darwin wrote to his friend and mentor Dr Hooker saying, in part, “I have long regretted that I truckled to public opinion, and used the Pentateuchal term of creation, by which I really meant ‘appeared’ by some wholly unknown process. It is mere rubbish, thinking at present of the origin of life; one might as well think of the origin of matter.”<sup>1,2</sup> Surprisingly, what Darwin thought to be the harder of the two problems—the origin of matter—was the sooner explained. In 1905 Albert Einstein published his Special Theory of Relativity, including his famous equation  $E = mc^2$ . Matter can be derived from energy (in accordance with the laws of quantum physics) and vice versa. It was the origin of life that turned out to be the harder problem.

Today, the origin of life, together with the finely tuned universe that supports it, has to be likewise traced back to the quantum world. Some claim that universes can emerge from quantum fluctuations within ‘nothing’ (a quantum vacuum).<sup>3</sup> I doubt this. But I do not doubt the recent discovery that life depends crucially upon quantum technology.<sup>4</sup>

However, in this article we don’t need to know anything at all about where things come from because I want to focus solely upon the results—life and the universe. If universes and life can arise from any naturalistic cause whatsoever, then they will continue to arise whenever those same causes continue operating. If they don’t continue to arise it must mean they only happened once. Things that happen just once are called singularities, and we can use the laws of probability to search for them. The evolutionary worldview relies from beginning to end on singularities, and when we

apply probability theory to look for them, we find that they don’t exist.

## Problems with probability

Physicist Stephen Hawking said in his ‘masterpiece’<sup>5</sup> *A Brief History of Time* that it is possible (though unlikely) for the molecules of gas in a sealed box to all move down one end and occupy only one half of the box. “The probability ... is many millions of millions to one, but it can happen.”<sup>6</sup> This is not true. Dr Hugh Ross, founder of Reasons to Believe, fell into the same trap<sup>7</sup> so I shall use the scenario to illustrate some basic principles of probability theory.

Hawking’s first error was to put probability in apposition to an event in a way that implies the small but finite probability caused or gave reason for the event to occur. But chance is not a force that can do things, and probability is nothing more than a set of theoretical tools that humans have developed to help them make decisions about uncertain events. A good decision is one that avoids ‘false positive’ outcomes (a Type I error) and ‘false negative’ outcomes (a Type II error). For example, if a medical test says you have cancer when you don’t (a false positive) it can cause unnecessary anxiety and expensive, wasteful, medical treatment (with potential associated negative side effects). But if the test says you don’t have cancer when you do have it (a false negative) it may put your life in danger. Doctors use the history of such tests to do probability calculations to help them make the best decision. If a *confident* decision cannot be made they will recommend further testing.



A basic rule of probability is that  $p = 1 - q$ , where  $p$  is the probability that an event will happen, and  $q$  is the probability that it will not happen. The Null Hypothesis (simplest assumption) in statistical testing is that there is no difference between some test measure and zero. If this assumption is proven false (at some calculated level of *confidence*) then the Alternate Hypothesis is accepted that it is different from zero. As the value of  $p$  becomes smaller, the value of  $q$  becomes larger, so a *confident* decision must strike a balance between Type I and Type II errors. The tables in the back of statistical textbooks carry a set of  $p$  values that optimize these risks, usually  $p = 0.05$ ,  $0.01$ , and  $0.001$ . Hawking's own probability statement gives us a value of  $p < 0.000000000001$ , and we will see shortly that it is not significantly different from zero. We should place *no confidence* in his reasoning, even by his own criteria.

But astonishingly, Hawking vastly underestimated the size of his problem. To understand why, we need to simplify his scenario. Suppose his box has just one molecule of gas in it and that in order to examine the contents we insert a partition at the half-way point so the molecule is either in the left (L) or right (R) hand end. There is a 100% probability that the gas molecule is either in L or in R. Add a second gas molecule, and to calculate combinations we must now label them, say A and B. The possible combinations are: (underlined groups signify all in one end) [A & B in L], [A & B in R], [A in L & B in R], and [B in L & A in R]. So the probability of both molecules being in one end only is two cases out of four, or 50%. Add a third molecule, C, and we get these combinations: [A, B & C in L], [A, B & C in R], [A & B in L & C in R], [A in L & B, C in R], [A, C in L & B in R], [B in L & A, C in R], [B, C in L & A in R], [C in L & A, B in R]. The probability is now two cases in eight, or 25%. Add a fourth molecule and the probability drops to 2 cases in 16, or 12.5%, and so on. The results are plotted in figure 1.

The pattern that emerges is that there are always only two possibilities of Hawking being correct (all in L or all in R), while the number of possible combinations rises as  $2^n$  where  $n$  = the number of gas molecules. The Binomial distribution describes this situation where one of two outcomes is possible. It shows that with 10 molecules  $p = 0.001$ , and with 20 molecules  $p = 0.000001$ . However, a shoe box of ordinary air would contain something in the order of  $10^{23}$  (a hundred thousand million trillion) molecules of gas. So the probability of Hawking being correct is not "many millions of millions to one" but just two chances in  $2^{100,000,000,000,000,000,000,000}$ , or about 1 chance in  $10^{30,000,000,000,000,000,000,000,000}$ . Since there are only about  $10^{80}$  atoms in the universe, Hawking's decision to say "it can happen" is an excruciating Type I error!

But there is a much more fundamental error in Hawking's scenario. The movements of gas particles are not chance events; they are determined by the laws of motion.

Probability theory can be applied to such events only as an approximation to physical reality. Chance cannot accomplish what the laws of physics prohibit. Being a physicist Hawking should have asked himself whether the laws of physics would permit such a scenario. The first law of motion says a body that is moving or at rest will continue in that state unless a force acts upon it. At normal room temperature and pressure the gas molecules—mostly nitrogen ( $N_2$ ) and oxygen ( $O_2$ )—zip around at more than a thousand miles per hour,<sup>8</sup> bouncing about like billiard balls on a billiard table but in 3-dimensions.

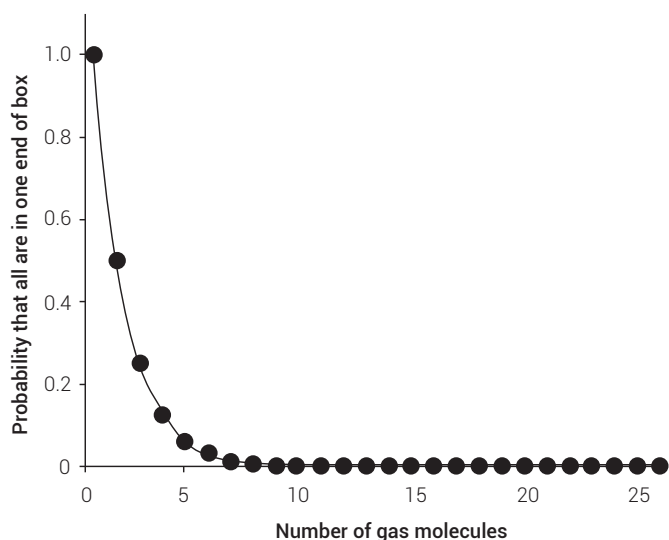
Suppose that gas molecules did begin to concentrate down one end of Hawking's box. Molecules in the transition region between the dense region and the empty region will face numerous obstacles if they move towards the dense region. They will bounce around among lots of other gas molecules adding to the pressure and temperature in that end. On the other hand, molecules that move towards the empty region will face no such resistance, so trillions of them will always be zipping back into the empty region at over a thousand miles per hour. Hawking's scenario could never eventuate.

People often apply probability theory inappropriately and an entertaining overview is presented in David Hand's book *The Improbability Principle: Why coincidences, miracles, and rare events happen every day*.<sup>9</sup> But in trying to explain everything with chance, Hand falls into the same trap as Hawking and Ross by applying probability theory to imaginary events that are divorced from physical reality. Astrobiologists make their living doing this very same thing. They 'guesstimate' a multitude of probabilities and insert them into the terms of the famous Drake equation to calculate the number of extraterrestrial intelligent civilizations in our galaxy and universe. Such applications are purely imaginary—using chance as a surrogate for ignorance—without proper regard for whether the proposed events are physically possible.<sup>10</sup>

## The singularity problem

As stated, a singularity is a unique event that only happens once. Singularities must have special causes, not common causes. Things that have common causes produce common events, not singularities. For example, rain is a common event (in most places on Earth) caused by particular aspects of the hydrological cycle. Rain generally falls downwards, not upwards, because gravity generally pulls things towards the centre of the earth. If rain is ever observed to move upwards, then it can usually be explained by an updraft in air currents—another facet of planetary climate.

In physics, a gravitational singularity occurs in the heart of a 'black hole'. When a large star burns up all its nuclear fuel it collapses in on itself, and it is a prediction of Einstein's



**Figure 1.** Probability that all gas molecules will accumulate in one end of Hawking's box, plotted against the number of molecules in the box.

General Relativity that its internal self-gravitational attraction overcomes all resistance to its core collapsing, thereby sucking everything nearby (including light, thus the name 'black hole') into a black hole with a singularity at its centre. This is a single point with density and temperature approaching infinity in an infinitesimally small volume, according to the theory. Once this happens there is no way of reversing it. This kind of event can happen many times because there are many large stars, but it can only happen once to a particular star because it is irreversible, on the timescale commonly assumed for the universe.

In mathematics, a singularity is a point in a given algebraic function where the derivative (rate of change) is undefined, but every near-neighbourhood point does have a derivative. This kind of singularity is somewhat like a sheet

of metal along which the algebraic function describes straight lines, but at a particular point there is a hole (a singularity) across which it is *not* possible to travel in a straight line.

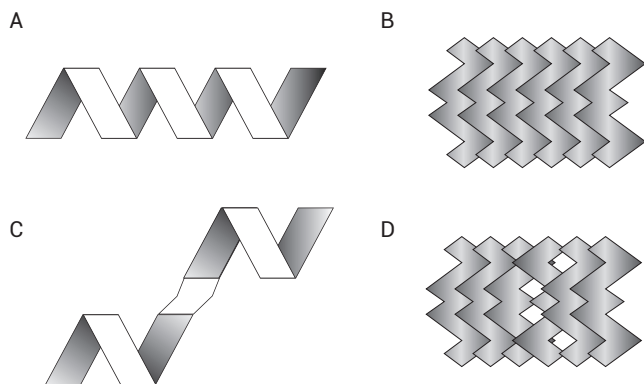
Singularities in the biochemical evolution of life on Earth were drawn to popular attention by Nobel Prize-winning biochemist Christian de Duve in his excellent book *Singularities: Landmarks on the Pathways of Life*.<sup>11</sup> He used the word 'singularity' to describe all the many barriers to progress in the development of life for which we currently have no naturalistic explanation. His first example was *homochirality* and it provides us with an easy way to illustrate the singularity principle.

### Homochirality

Life's molecules are generally 100% pure in their chemical composition. In contrast, environmental materials such as air, soil, and water are always mixtures of many different chemicals.<sup>12</sup> Life is built upon carbon-based molecules and many of these have a property called *chirality*—they can exist in two forms that are mirror-images of each other (like our left and right hands) and these are called *enantiomers*. Cells generally use only 100% pure forms of just one of the two enantiomers (e.g. left-handed amino acids and right-handed sugars).<sup>13</sup> Such 100% pure forms are said to be *homochiral* (of the same *chirality*).

Laboratory experiments that produce amino acids and sugars always produce an approximately 50:50 mixture of the left- and right-handed forms. Likewise, amino acids that have been found in meteorites are mixed. The problem that Christian de Duve faced was how to turn a 50:50 mixture into a 100% pure version of just one—and always the same—enantiomer. There is no known way of doing it in an environmental setting because both enantiomers have the same chemical properties. It can only be done in the laboratory with specialized equipment.

The reason that cells *must* use *only* homochiral molecules is illustrated in figure 2. The *primary structure* of a protein is expressed in its sequence of amino acids. Its *secondary structure* is expressed in the way the long protein chain folds up to make a functional piece of molecular material that can then be formed into a molecular machine. The most common folding patterns are the *alpha-helix* (figure 2A) and the *beta-sheet* (figure 2B) forms. These patterns are possible only if *every* amino acid joins up in exactly the same way. The *alpha-helix*, for example, will continue turning around on itself in a symmetric helical pattern only if every single unit within it follows the pattern.<sup>14</sup> If just one right-handed amino acid is included, then the symmetrical pattern of the *alpha-helix* is disrupted



**Figure 2.** Homochirality is essential in maintaining the correct secondary structure of proteins. The homochiral alpha-helix (A) and beta-sheet (B) are both made of 100% left-handed amino acids. If even one right-handed molecule is present, it destroys the helix (C) and creates a defect in the sheet (D).

(figure 2C). Likewise, if even one right-handed molecule is included in the *beta-sheet*, then it causes a defect in the material (figure 2D).

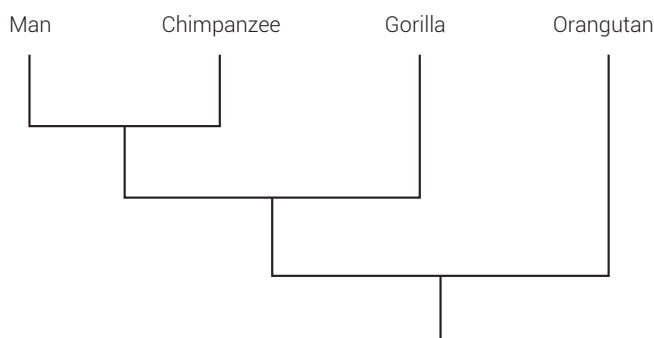
Stanley Miller's pioneering 1953 origin-of-life experiments used electricity to simulate lightning strikes in gas/liquid mixtures and produced some trace amounts of useful amino acids. However, such experiments create more problems than they solve. They produce a mucky mess containing many more useless chemicals than originally present,<sup>15</sup> so the system is much further away from the 100% purity that life requires!

Homochirality is just one of the many kinds of problems that de Duve faced over and over again throughout his book. He did an excellent job of making suggestions on how to overcome these barriers, but in the end had to admit defeat. Something very special indeed must have happened to produce each one of the extraordinary and varied outcomes that he listed among life's basic requirements—things that no-one has ever observed to happen in the natural world. That is why he called the book '*Singularities*'.

### Singularities, miracles, and universes

Singularities present evolutionists with a severe, but generally overlooked, problem. Because singularities only happen once they are indistinguishable from miracles. A miracle, according to the American Heritage Dictionary of the English Language, is "An event that appears inexplicable by the laws of nature and so is held to be supernatural in origin or an act of God". De Duve's list of singularities included all the major components of the first prokaryote cell, plus those of the first eukaryote cell, plus the requirements for multi-cellularity, right up to the origin of man. However, singularities are not just confined to biochemistry—they are *everywhere* in the evolutionary worldview, right back to the origin of the universe.

The big bang theory of the origin of the universe begins in a gravitational singularity. There is no way to get a universe out of such a singularity, so the supposed 'big bang' event had to have been another singularity. The imagined subsequent history was recently summarized by a group of expert critics as consisting of: General Relativity Theory + Dark Matter + Dark Energy + Inflation.<sup>16</sup> The latter three of these four are purely imaginary, and General Relativity Theory fails when applied to spiral galaxies and galaxy clusters so it cannot be trusted to describe the whole universe. These critics seriously suggested adding a further imaginary 'Dark Force' to the theory to get it working better! Creationist expert John Hartnett has shown that Carmeli's Cosmological Relativity



**Figure 3.** A tree diagram of Hominid evolution, based on DNA sequence comparisons. Redrawn from Lecointre & Le Guyader, *The Tree of Life*, 2006.

Theory can produce better explanations that do not need such imaginary components.<sup>17</sup>

According to theory, the big bang fireball should have produced equal amounts of 'matter + anti-matter' (mostly hydrogen and anti-hydrogen) but the anti-matter has not been observed, so another singularity is required to make it 'disappear'. Then another 'monster universe' of 'cold dark matter' (many times the size of the big bang) had to have come into being by some entirely unknown singularity. Then by another singularity the cold dark matter spontaneously organized itself into countless galaxy- and star-sized clumps, which could then gravitationally pull the expanding cloud of matter-gas into the clumpy stars and galaxies that we see today, as far as our telescopes can reach. This theory doesn't work when applied to our local group of galaxies so it certainly should not be trusted to explain the universe.<sup>16</sup>

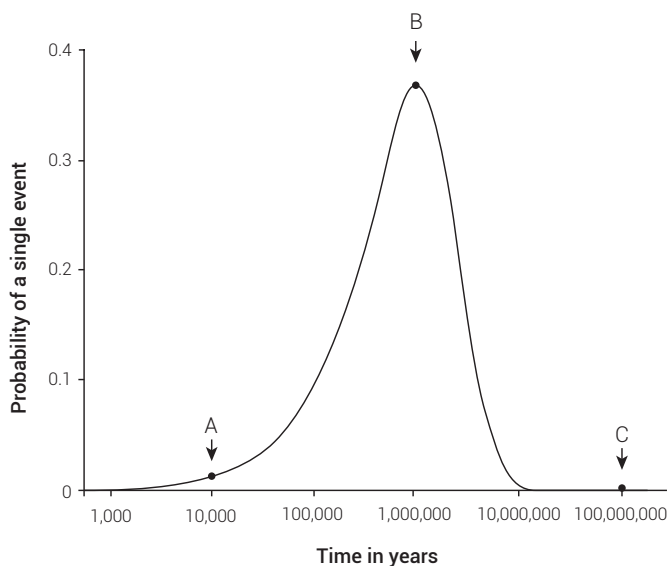
Planet formation "still suffers from a large number of unsolved mysteries" and it requires multiple singularities to explain why every known planetary system is different.<sup>18</sup> Even the very first step—the accretion of stardust—faces a "seemingly unsurmountable 'meter-size barrier' for the growth of particles".<sup>19</sup> Most scientists give the impression that they can explain the whole universe with science, but the more we get to know about it, the more miraculous it appears.

### Singularities everywhere

A large catalogue of singularities confronts us in the phylogenetic trees that adorn textbooks on evolutionary biology. Consider the example of the Hominid tree in figure 3.

Christian de Duve highlighted the problem in these diagrams with questions such as: Why did only one line of hominids lead to modern man? Why did only one line of fish develop lungs and walk onto land and become amphibians? We could add to his list by asking: Why did only one line of amphibians turn into reptiles? Why did only one line of reptiles turn into birds? Why did only one line of reptiles





**Figure 4.** The probability of just one evolutionary event occurring during a range of different times, when its expected frequency is once in a million years, according to the Poisson distribution.

turn into mammals? Why did only one line of mammals turn into primates?

Another approach to the problem is via ‘Murphy’s Law’. Murphy’s Law says that if anything can go wrong it will. It arose in the field of marine engineering design. Design engineers need to build safety factors into their designs to deal with all the possible things that can go wrong. This is especially important in shipbuilding because if something goes wrong at sea, people die. Design engineers therefore need to expect the worst to happen, and then design their structures in the full knowledge that if something can go wrong it will.

A more positive statement of this principle is that ‘if something can happen, then it probably will happen eventually’. Singularities become problematic for evolutionists when they claim that their stories only appeal to natural causes and repeatable random events. We then have to ask, “How often will it happen?” If it can happen once in a million years (or 5 or 10 million years), then it could have happened a multitude of times in the 600 million years currently assigned to the reign of multicellular life on Earth. Singularities become impossible in this timeframe!

### Probability of single events

We can use probability theory to estimate the likelihood that an evolutionary event will happen just once and only once. That is, if an event can happen and it does happen, then, like rain falling or stars exploding, it may happen more than once. On the other hand, if it is to qualify as a singularity,

then we need to know the probability of it happening just once and only once.

For single random events that occur at variable time intervals, the Poisson distribution can tell us, for a given expected frequency of occurrence, how often an event is likely to occur during a given time interval. For example, if someone claims that a particular kind of evolutionary event can occur once in a million years, then we can use the Poisson distribution to calculate the probability that it might occur 0, 1, 2, 3, or 10, or any other number of times during any particular time period. We can also use the Poisson distribution to find the probability of an event occurring just once during different lengths of times, as plotted in figure 4. In this case there is a small probability that it could occur once in ten thousand years (point A). It is most likely to occur just once after a million years (point B). However, after a hundred million years the probability is zero (point C) because it would have occurred many times by then.

Now let’s see what the probabilities are for various numbers of events at any given time. Figure 5 shows the probability curve for the expected number of evolutionary events after 10 million years when the expected frequency is once in a million years.

This graphs shows why singularities are so troublesome when the timescale is greater than the time needed for the event to occur once. If an evolutionary event can occur once in a million years, then after 10 million years it is most likely to have occurred 10 times (point B). The probability of it occurring 20 times (point C) at  $p = 0.002$  is four times greater than the probability of it occurring just once (point A) where  $p = 0.0005$ .

### Probability of multiple singularities

Singularities are not the greatest problem facing evolutionary biology—an almost infinitely greater problem is how to deal with long series of singularities! Take, for example, the lineage that supposedly led from single-celled ancestors to humans. In his book *The Ancestor’s Tale: A Pilgrimage to the Dawn of Evolution*, Richard Dawkins traced the evolutionary history of humans backwards through time. He estimated that there were about 40 critical evolutionary events required to turn the single-celled ancestor into a human.<sup>20</sup>

Now there are some differing opinions among evolutionary biologists over particular transition points, and opinions change as new fossils are discovered. But in general, at any one time, the consensus is usually that one particular fossil (or fossil species) represents the best evidence of the transitional form or common ancestor. That is, if a fossil is known, then biologists tend to be satisfied with that and do

not require a multitude of ancestors—it is simply assumed that one is both necessary and sufficient. Dawkins followed this reasoning, and his uniformitarian worldview allowed only one kind of driving mechanism for the evolutionary process—what we see happening around us today, mostly natural selection of natural variation.

There are differing time intervals between Dawkins' 40 critical events, but for the sake of simplicity let's just take the average length of time and call it  $T$ , so that the whole sequence would require a total time of  $40 \times T$ . Using the method illustrated in figure 5 for single random events we can see that the first evolutionary event should have taken place about 40 times by now. That is, if such an event can occur once in time  $T$  then it should occur, on average, about 40 times during a period of  $40 \times T$ . Similarly, the second event should have occurred about 39 times, the third about 38 times, the fourth about 37 times and so on. Only the last evolutionary event in the series would be expected to have occurred just once. That is what we would expect to happen, on average. What is the likelihood that each of the 40 steps occurred just once, and only once?

When we go to a shop and buy multiple items, the total amount we pay is the sum of the prices for each individual item. The order in which the items are entered into the register doesn't matter. However, with probabilities like this series of 40 events we must *multiply* the probabilities because each event is dependent upon the event preceding it. So the probability that all events will occur just once is the probability of getting just one event when 40 are expected, multiplied by the probability of getting one event when 39 are expected, and so on. The result is such a tiny number (1 chance in  $10^{308}$ ) that there are not enough atoms in the universe to make it happen. It simply cannot happen. If we now bring this argument back to Dawkins' *Dawn of Evolution*, the first event after the origin of life was a transition from one (unknown) to two fundamentally different types of prokaryotic life (bacteria, archaea). If such a transition really can occur naturalistically, then we should today see something like 40 fundamentally different types of prokaryotic life. Since we don't see this (and we could elaborate this reasoning through all 40 steps) we can conclude that probability had nothing to do with it.

### The origin of species

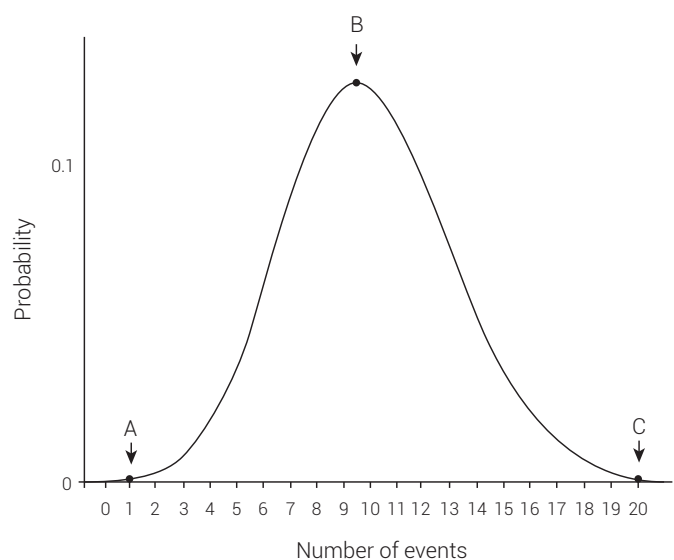
One obvious rejoinder to this calculation is that speciation usually occurs via populations, and populations can number in the millions. Only rarely does a new species arise from a single founding individual. Jean-Jacques Kupiec argues that the fundamental realities in biology are not species, but individual

lineages. Each one is different from every other, and it is the collective histories of individuals that we should be studying rather than trying to squeeze them into man-made categories.<sup>21</sup> If Dawkins' 40 crucial events happened to multitudes of variable individuals at any one time, then his problem with singularities would disappear.

But Charles Darwin faced a similar problem when he looked at the fossil record. If his theory had been correct—that all species had evolved from other species via long sequences of small changes—then the fossil record should consist of endless examples of transitional forms. But the fossil record is *not* like that. It shows that species usually appear fully formed, and remain much the same throughout their history. Gaps are real. Palaeontologist Stephen Jay Gould called this 'the central fact of the fossil record'.<sup>22</sup>

In similar manner, if Kupiec's theory is correct, then we should expect to see endless examples of transitional forms among living organisms today. In general this again is *not* what we see. Most organisms fit fairly well into their species categories. Yes, there are continuous and widespread variations, but humans are very easily distinguished from their nearest supposed relatives, the chimpanzees and gorillas. Taxonomists do have problems trying to sort out a few notoriously variable species complexes but most species are usually clear-cut and non-problematic once they have been studied and described in adequate detail.

In contrast, Dawkins' 40 transitional events were not species-level transitions. The first half of his list consisted of the largest 'jumps' of all across the highest levels in the taxonomic hierarchy—the phyla! According to leading experts, the origin of the multi-cellular phyla in the



**Figure 5.** The likely numbers of evolutionary events after 10 million years, when the expected frequency is once in a million years, according to the Poisson distribution.

Pre-Cambrian era poses a severe challenge. Smithsonian palaeontologist Douglas Erwin called it a conundrum.<sup>23</sup> Caltech developmental biologist Eric Davidson said that the differences between the phyla are due to unchanging upper-level control circuits that are conserved in all descendants. “A strong conclusion ... is that the evolutionary process generating the [animal] body plans was in many ways very different from the evolutionary changes that can be observed at the species level in modern animals.”<sup>24</sup> These experts are telling us that they cannot explain the big differences.

The second half of Dawkins’ transitional events covers the evolution story from fish to humans. Among these transitions the smallest step is the most recent one—the origin of humans from an ape-like ancestor. No-one has any idea how or why one lineage of apes changed into humans while the others remained as apes. And the timescale of human genome decay, even as acknowledged by leading evolutionary geneticists, shows it cannot possibly have survived for the supposed multiple millions of years required for this transition.<sup>25</sup> Since this smallest of all steps remains a singularity, then all of the larger steps preceding it also qualify as singularities, and Dawkins’ problem remains unsolved.

## Conclusion

The entire evolutionary worldview—from the origin of the universe to the origin of the human intelligence that contemplates it—consists of a series of singular events that are indistinguishable from a multitude of miracles. Scientists cannot study singular events, only repeatable ones. But when evolutionists claim that the evolutionary process is naturalistic, repeatable, and a product of chance, then we can use the laws of probability to test that claim. It turns out to be impossible. But evolutionists are not the only ones with this problem. Everyone who has a story of origins (the Bible included) will find it consists of the same thing—a long series of singular events. The big question, therefore, is which one (if any) is correct? There is widespread evidence in creationist literature supporting the biblical account. But regardless of evidence, this singularity problem is a reminder to all of us that origin stories are not primarily based on science, but on worldview.

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12. There are some very rare exceptions. A few elements can occur in pure solid form in mineral deposits (e.g. native copper and native silver).
13. One notable exception to this rule is that bacteria use right-handed amino acids to strengthen their cell walls with cross-bracings.
14. There are 20 different amino acids used in making proteins. They have different sizes and shapes and are arranged in different sequences so the outer contours of a protein may be quite irregular, but the way that the amino acids link up is the same and this creates the symmetry of the core structure.
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# Textual traditions and biblical chronology

*Lita Cosner and Robert Carter*

There are three major textual traditions for the chronogenealogies of Genesis 5 and 11: the Masoretic text (MT), the Samaritan Pentateuch (SP), and the Septuagint (LXX). Comparisons of the three texts side-by-side show some important differences. The number and types of changes made to the texts by ancient scribes is most easily explained if the SP and LXX deliberately manipulated the chronological numbers in specific ways, causing date inflation and downstream chronological difficulties. Many changes are demonstrably deliberate, for they involve changing two numbers simultaneously, and all the differences occurred within the chronogenealogies themselves, not in the data for the individuals that link the two or for those that extend beyond the second. Most significantly, a single change to Jared's age when Enoch was born from 162 to 62, shared by the SP and proto-LXX, appears to have had a cascade effect, causing multiple patriarchs to be recorded as living past the Flood. The scribes involved in copying these texts were aware of the problem. The LXX translators seem to have inflated their text and left only the death of Methuselah post-Flood. The SP tradition seems to have truncated the lifespans of Jared, Methuselah, and Lamech to make them all die in the Flood year. Taking the various text types into consideration, the Masoretic seems to most closely reflect the original reading in the Genesis 5 and 11 genealogies.

For the biblical creationist, the genealogies in Genesis 5 and 11 are foundational for constructing any timeline of Earth history. There are multiple textual traditions and one's chronology will be determined by the text one chooses to follow. However, it is possible to examine the three major textual traditions and arrive at a reconstruction of the textual history that both honours the biblical text and makes sense from a text-critical perspective.

## The relevant textual traditions

The Masoretic text (MT) is the basis for most English translations of the Old Testament today and is widely regarded as the best-preserved text of the Hebrew Bible. Yet, the oldest extant manuscript is dated to around AD 900, and we cannot simply assume that its genealogical figures are the most accurate without further investigation. Interestingly, the Latin Vulgate follows the MT exactly for the figures in question, meaning the MT tradition must date at least back to the translation of the Latin text, several hundred years earlier than the oldest surviving MT manuscript.

The Samaritan Pentateuch (SP) is also known only through manuscripts from the Medieval period; the earliest manuscript dates to the tenth century. It differs from the MT in about 6,000 places and agrees with the Septuagint (LXX) in about 2,000 of those places.<sup>1</sup> While it was obviously and intentionally changed to align with Samaritan practices—most notably with the addition of a commandment to build an altar on Mt Gerizim—most scholars agree that it bears witness to an ancient textual tradition.

The LXX refers to a family of ancient Greek texts of the Old Testament. The earliest and most complete copies are preserved in the Christian 'great uncials' Sinaiticus, Vaticanus, and Alexandrinus, though there are LXX fragments dating as far back as the first century BC, and the New Testament gives many quotes of LXX passages, testifying that those particular readings date at least to the first century AD. Most scholars, whether 'liberal' or 'conservative', view its version of the Genesis 5 and 11 chronologies as clearly secondary, a recension (a deliberate editorial revision of a text) possibly to agree with the Egyptian chronology of Manetho.<sup>2</sup> In fact, Wenham goes so far as to say, "Which of these chronologies is closest to the original? There is no consensus on this issue, except that the LXX looks secondary."<sup>3</sup> Even though it is widely acknowledged that the term 'Septuagint' does not refer to a single monolithic entity, the various LXX texts do not have significant variants in the Genesis 5 and 11 genealogies.

## The relevant passages in Genesis

The genealogies of Genesis 5 and 11 have been called 'chronogenealogies' because they contain more than just a list of names; they also provide the age of the father when his son was born, allowing us to construct a proper timeline. Genesis 5 also provides a total lifespan for each patriarch, which serves as a checksum. This important detail constrained the changes (deliberate or otherwise) ancient scribes could have made to the text.

Genesis 5:1–32 contains a list of Adam's descendants through his son Seth to Noah's sons Shem, Ham, and Japheth.

Each patriarch's age at the birth of his son is listed, followed by the remainder of his lifespan, and finally his total lifespan. This formula repeats through the entire section in each text type.

Genesis 11:10–26 contains a list of the descendants of Noah's son Shem to Terah's sons Abram, Nahor, and Haran. Each patriarch's age at the birth of his son is listed, followed by the remainder of his lifespan. The Samaritan Pentateuch adds the total lifespan to the end of each patriarch's entry.

It is possible to bridge the two passages in order to create a single chronogenealogy. Genesis 8:13 tells us that the Flood came when Noah was 600 years old and Genesis 11:10 reports that Shem was 100 when Arphaxad was born and that this happened two years after the Flood. This means that Shem was 98 when the Flood came and Noah was 502 when Shem was born (ignoring some of the ambiguities inherent in the text).

We can also extend the chronology to include the lives of Abram, Isaac, Jacob, and Joseph. However, there is an ambiguity involving the age of Terah when Abram was born. Ussher and many others argue that Terah was 130 when Abram was born, because Terah died at the age of 205, after which Abram left Haran at the age of 75 (Genesis 11:32; 12:4). However, the text only says that Abram was old enough to be married to a wife 10 years younger (Genesis 17:17) before the family moved to Haran (Genesis 11:31). There may have been a period of time between Terah's death and Abram leaving Haran, up to possibly 50 years.<sup>4</sup>

Genesis 21:5 establishes that Isaac was born when Abraham was 100 years old. Genesis 25:26 states that Isaac was 60 when Jacob and Esau were born. Joseph was 17 when he was sold into slavery (Genesis 37:2) and 30 years old when he became the vizier of Egypt (Genesis 41:46). Between 30 and 37, Joseph fathered his sons Manasseh and Ephraim (Genesis 41:50). Nine years after attaining the viziership, he called his family to Egypt when Jacob was 130 (Genesis 47:9). Combining these figures allows us to conclude Jacob fathered Joseph when he was 91 years old.

And thus, we can construct a biblical chronology that includes 23 consecutive generations, from Adam to Joseph. Importantly, although textual differences have arisen in the Genesis 5 and 11 chronogenealogies, there are no differences in the isolated dates that allow us to bridge between them, nor in the additional chronological information about Abraham, Isaac, Jacob, and Joseph. This is a strong clue that many of the changes that were made to the chronogenealogies were, in fact, deliberate.

Taken straightforwardly, the genealogies of Genesis 5 and 11 present a chronological framework with no gaps. Even if there were gaps in the generations represented in the genealogies, the age of the ancestor at the birth of his descendant is not dependent on whether that descendant

is his son or his great-great grandson (though all evidence points to straightforward father-son descent).<sup>5</sup>

## Genesis 5

As mentioned above, all extant manuscripts are late compared to the original composition date of Genesis. The various traditions also diverged centuries prior to any documentary evidence but the overall similarity of the texts bears witness to the care taken in copying the manuscripts. Because it is the basis for all English Bible translations, the MT will be used as a baseline for comparison; however, this is only for convenience and does not *assume* the superiority of the MT genealogy.

There are many reasons why the majority of scholars believe the LXX and SP share a common textual source. The similarity in Methuselah's age at the birth of Lamech in the SP (67) and the LXX (167, 'inflated'—see below for definition) is one reason (of many) for this. Yet, the SP and MT have the same basic framework for most of the men in this list while the LXX differs more widely, which seems to indicate the changes were made later.

Compared to the MT, in Genesis 5 the LXX generally inflates the age of the father at the birth of his son by 100 years and subtracts 100 years from the remainder, keeping the total lifespan the same (table 1). Thus, it appears the inflated LXX ages occurred after the fact, perhaps at the time of translation. In other words, these changes are systematic and deliberate and the checksum was in the common textual tradition predating all three texts. Whoever made the changes in the LXX had to adjust two different numbers in each person's entry in order to inflate the chronology while keeping each patriarch's lifespan the same, meaning this was no simple scribal error.

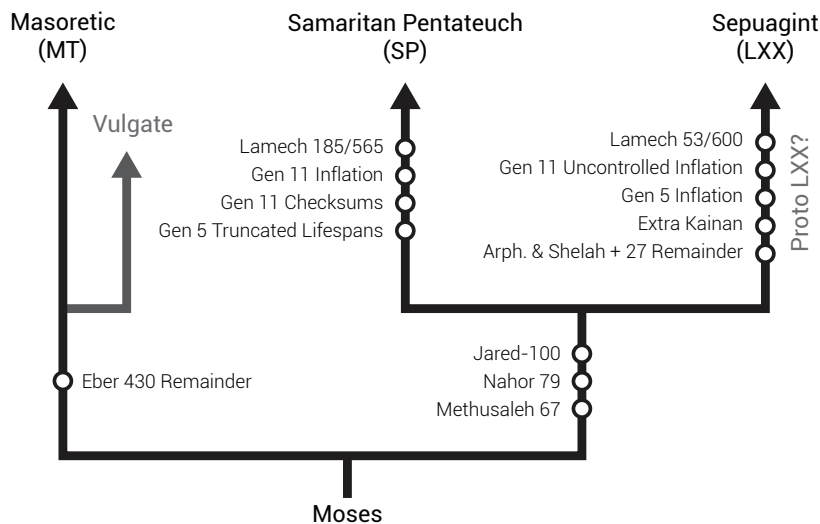
If we assume this inflation was consistent and intentional, we can reverse the process to arrive at a 'proto-LXX' reading. These adjusted ages agree with the MT exactly for the first five generations. The first divergence is Jared's age at the birth of Enoch. The adjusted age would be 62 (agreeing with SP), rather than the listed 162 which agrees with the MT. The checksum for Jared is identical in both the MT and LXX, so either the LXX left it as in the original because it fits the general pattern of the generations around it or Jared somehow lost 100 years in the common LXX-SP text tradition. The latter is more likely as it requires fewer steps and less deliberate action on the part of the copyists and/or translators (figure 1).

Enoch's adjusted entry in the LXX genealogy agrees exactly with MT but the entries for Methuselah and Lamech differ wildly in the three texts. Of course, the primary problem with the (Hebrew) proto-LXX is that Jared, Methuselah, and Lamech would live well past the Flood!

**Table 1.** Comparison of the Genesis 5 and 11 chronogenealogies in the Masoretic (MT), Septuagint (LXX), and Samaritan Pentateuch (SP). Light grey = unique readings in LXX or SP. Dark grey = places where SP and LXX agree against MT. Dotted lines separate the main chronology from transition persons whose data must be calculated. It takes careful cross-referencing to tabulate the data for some individuals. For example, Joseph was 30 when put in charge of Egypt, + 7 years of plenty, + 2 years of famine, + Jacob was 130 when he went before Pharaoh. Therefore  $130 - 7 - 2 - 30 =$  Jacob was 91 when Joseph was born. He lived in Egypt for 17 years, therefore, Joseph was 56 when Jacob died. Similar care must be taken when figuring the link between Noah and Arphaxad and between Terah and Abraham.

Person	Generation	References	Masoretic (MT)			Septuagint (LXX)			Samaritan Pentateuch (SP)		
			Age at son	Re-main-der	Age at death	Age at son	Re-main-der	Age at death	Age at son	Re-main-der	Age at death
Adam	1	Gen 5:3-5	130	800	930	230	700	930	130	800	930
Seth	2	Gen 5:6-8	105	807	912	205	707	912	105	807	912
Enosh	3	Gen 5:9-11	90	815	905	190	715	905	90	815	905
Cainan	4	Gen 5:12-14	70	840	910	170	740	910	70	840	910
Mahalalel	5	Gen 5:15-17	65	830	895	165	730	895	65	830	895
Jared	6	Gen 5:18-20	162	800	962	162	800	962	62	785	847
Enoch	7	Gen 5:21-23	65	300	365	165	200	365	65	300	365
Methu-saleh	8	Gen 5:25-27	187	782	969	167	802	969	67	653	720
Lamech	9	Gen 5:28-31	182	595	777	188	565	753	53	600	653
Noah	10	Gen 5:32, 8:13-14, 9:28	502	448	950	502	448	950	502	448	950
Shem	11	Gen 11:10-11	100	500		100	500		100	500	600
Arphaxad	12	Gen 11:10-12	35	403		135	430		135	303	438
Cainan		(Gen 11:14-15)				130	330				
Shelah	13	Gen 11:14-15	30	403		130	330		130	303	433
Eber	14	Gen 11:16-17	34	430		134	370		134	270	404
Peleg	15	Gen 11:18-19	30	209		130	209		130	109	239
Reu	16	Gen 11:20-21	32	207		132	207		132	107	239
Serug	17	Gen 11:22-23	30	200		130	200		130	100	230
Nahor	18	Gen 11:24-25	29	119		79	129		79	69	148
Terah	19	Gen 11:26, 32	>=130	<=75	205	>=130	<=75	205	>=130	<=75	205
Abraham	20	Gen 11:31, 12:5, 17:17, 25:7	100	75	175	100	75	175	100	75	175
Isaac	21	Gen 25:26, 35:28	60	120	180	60	120	180	60	120	180
Jacob	22	Gen 47:28, 41:46	91		147	91		147	91		147
Joseph	23	Gen 50:22, 26	< 37		110	< 37		110	< 37		110





**Figure 1.** A textual family tree showing a possible history of the three main Old Testament text types. This tree represents the most parsimonious history, meaning the fewest changes must be made to account for all the differences. Vertical scale is arbitrary and branch lengths do not represent number of differences.

But systematic date inflation in the LXX translation means that only Methuselah remains a problem (table 2). He notably lives for 14 years after the Flood. This error was corrected only in the later copies of LXX; early copies retain the error.

In the SP, the data for six of the nine patriarchs agree with the MT without any adjustment needed. As above, the entries for Jared, Methuselah, and Lamech display major differences. Here, the age at birth of the son, the remaining years of life, and the checksum are all different. The lifespan of the three patriarchs appears to have been truncated in the SP to cause them to die the year of the Flood. The broad agreement of the SP with the MT means that the two probably represent a superior text than the inflated LXX in Genesis 5.

### Jared

There is one possible early change that might explain almost all of these differences: the age of Jared when Enoch was born. The MT records the age as 162 and has no following chronological difficulties. However, the single change from 162 to 62, shared by the SP and proto-LXX, appears to have had a cascade effect causing multiple patriarchs to be recorded as living past the Flood. The scribes involved in copying these texts appear to have seen the problem and corrected the text in different ways. The LXX translators' inflation of their text left only the death of Methuselah post-Flood (figure 2, lifespan charts).<sup>6</sup> The SP seems to have truncated the lifespans of Jared, Methuselah, and Lamech to make them all die in the Flood year.

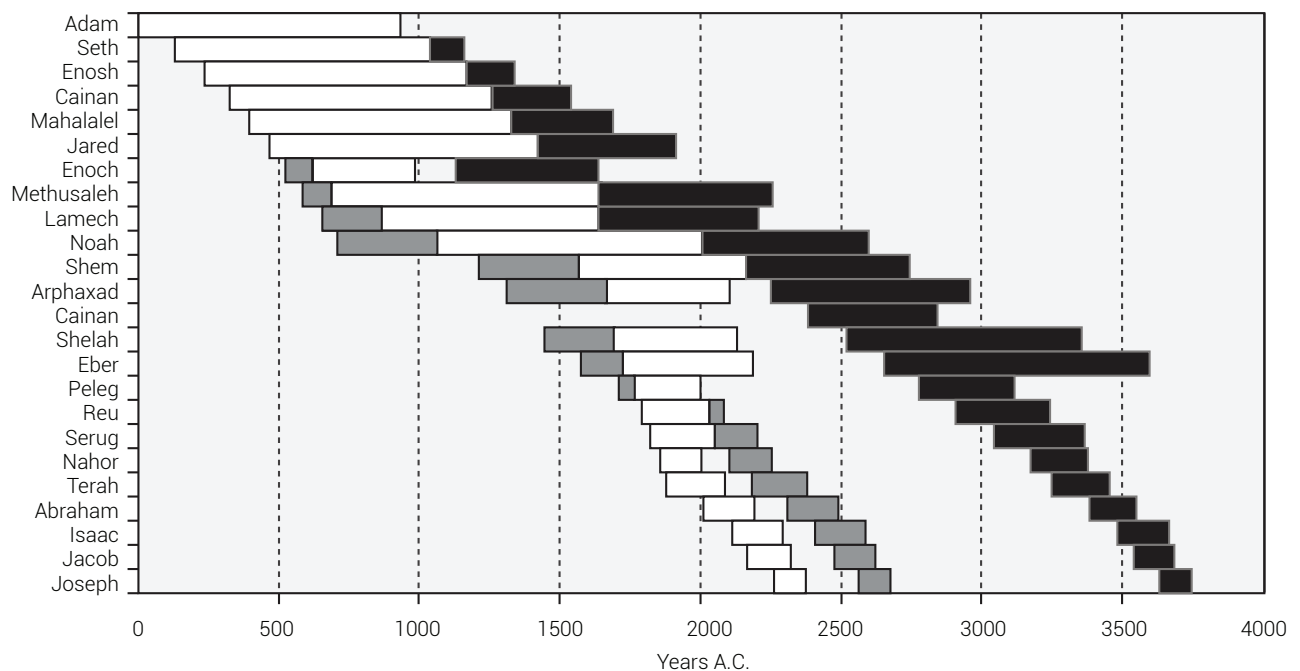
### Reconstructing a textual history for Genesis 5

In this reconstruction, we propose the MT preserves the correct chronology. This reconstruction is illustrated in figure 1. The reading of the MT, SP, and reconstituted 'proto-LXX' are very similar and the differences seem to be best explained as deliberate changes to the SP and LXX to get around chronological difficulties caused by earlier errors.

Due to the nature of textual criticism, it is impossible to say with certainty what the reading of the original text is concerning this datum for Jared. Therefore, we can only say that the MT appears to be a superior attempt to maintain the chronology, not that it conforms perfectly with the original. Given the textual variants that have been preserved, it appears that the MT preserves the original reading, therefore the LXX and SP

**Table 2.** The Genesis 5 genealogy in a theoretical 'proto-LXX'. With the exception of three patriarchs, 'proto-LXX' agrees with both the MT and the SP. Lamech, Jared, and Methuselah would live past the Flood if one used the 'simple additive' method for calculating dates and so we see more complex changes to their dates than in any other place within the chronogenealogies. Differences from MT bolded; asterisk indicates agreement with SP.

Patriarch	Age at son's birth	Remainder	Total lifespan	Year of death AM
Adam	130	800	930	930
Seth	105	807	912	1042
Enosh	90	815	905	1140
Kenan	70	840	910	1235
Mahala-leel	65	830	895	1290
Jared	<b>62*</b>	<b>900</b>	962	1422
Enoch	65	300	365	<b>887</b>
Methuselah	<b>67*</b>	<b>902</b>	969	<b>1556</b>
Lamech	<b>88</b>	<b>665</b>	753	<b>1431</b>
Noah	502	448	950	<b>1716</b>
Flood Year	<b>1342</b>			



**Figure 2.** Life history data for the first 23 biblical generations. The Masoretic chronology is shown in white and obscures the Samaritan Pentateuch (grey) and Septuagint (black) where they overlap.

can be explained as textual corruptions followed by editorial manipulation.

### Lamech

The one entry that is not explained by this reconstruction is that of Lamech. All three texts disagree (table 1) and the reconstruction is not obvious. While Klein dismisses the MT lifespan of 777 as “connected with the tradition about Lamech in Gen. 4”<sup>7</sup>, this is simply not the sort of change we see elsewhere in the MT and certainly not in this passage. While both LXX and SP are evidently recensions in general, all other evidence points to the MT being an attempt to transmit the text unchanged. For this reason, we prefer the MT’s figures for Lamech.

### Genesis 11

Compared to the MT, both SP and LXX include an inflated Genesis 11 chronology. However, the SP uniquely includes a total lifespan, which acts as a checksum and constrains the SP’s inflation in the same way as the checksum in Genesis 5 constrains the inflation applied to that passage by the LXX. The SP retains the same total lifespan as the MT for all nine patriarchs. This is best explained as an intentional harmonization to duplicate the formula in Genesis 5 and this is the sort of change the SP often makes. For example, in Exodus, what God tells Moses to say to Pharaoh in one place

is duplicated verbatim when Moses is speaking to Pharaoh, while the Masoretic tradition has small differences. This supports the contention that the SP is indeed a recension, since later copyists tend to harmonize rather than introduce differences.

However, the inclusion of the checksum enables us to untangle a textual knot. Even though the LXX has the same age inflation as the SP for the age of each patriarch at the birth of his son, the additive lifespans do not match. This means the SP started with a MT-like source, calculated the lifespans, and deliberately added the lifespans into the text as a checksum. Afterwards, they inflated the age of the patriarchs at the birth of their sons but the checksum forced them to truncate the remainder of the lifespan by the same amount as the inflation. The importance of this ‘controlled’ inflation cannot be overstated, for it is obvious that the SP and MT started with similar source documentation for Genesis 11. If the SP and LXX text types have a common ‘ancestor’, as the data suggest, this means the LXX would have also started with a MT-like source. Thus, the LXX inflation of Genesis 11 is late and purposeful. It was also ‘uncontrolled’ (i.e. without an added checksum).

### Eber

However, in the case of Genesis 11, there is evidence that the LXX preserves one number correctly which was corrupted in the MT tradition. For Eber’s entry, the SP

checksum and calculated proto-LXX lifespan match but the MT is 60 years off. The LXX and SP have predictably inflated the age-at-birth by 100 but we would expect LXX to maintain the remaining years of life and for SP to reduce it by 100 to keep the total lifespan the same. The 370 figure given in the LXX and the 270 given in the SP fit this formula but the MT gives 430. In fact, there is reason to believe that 370 is the original number. However, it should be noted that this has no effect on the MT chronogenealogy. As Klein explains:

“MT should be 370: its present reading results from a confusion with the age given for Eber at the birth of his first born ארבע ושלשים שנה [*‘arba’ ūsh’lōshīm shānāh*, four and-thirty years] and a subsequent metathesis: [מאות שנה] ושלשים שנה וארבע [*sh’lōshīm shānāh w’arba’ [me’ōt shānāh]*, thirty years and-four [hundreds years]].”<sup>8</sup>

### Nahor

Nahor’s entry is not as easy to explain. The SP checksum retains the total calculated from the MT (148), meaning this total value must have existed before the SP was composed. However, the SP and LXX give the same age when Terah was born (79), while the MT has 29. This would mean the SP inflated by 50 years instead of 100, as did the LXX.

There are only a few remaining differences among the main text types in Genesis 11 and none of them affect the chronology. The first is that the LXX adds 27 years to the remainder of Arphaxad and Shelah. While one might be tempted to think they simply switched two numerals (creating ‘430’ from ‘403’), it must be remembered that neither the original Hebrew text nor the Greek translation uses numerals in this way. In fact, the numbers are spelled out. The difference is the result of a simple scribal change in both cases, from the singular שלש (*shālōsh*, translated ‘three’) to the plural שלשים (*sh’lōshīm*, translated ‘thirty’).<sup>9</sup>

### Discussion

Is the LXX secondary? Why did the LXX translators inflate the genealogy?

The biggest difference in all the textual traditions is that the Septuagint gives a dramatically longer chronology than either the MT or the SP. We argue that this was an *intentional* change. There are multiple possible reasons why the LXX translators or copyists may have inflated the genealogies. One might be to avoid something that seems as strange to us as it would to them (Hendel called it ‘disturbing’<sup>10</sup>)—multiple overlapping generations. Klein explains a possible

motivation for inflation in Genesis 11 SP which also applies to LXX:

“Whatever the significance of the individual figures may have been, a person calculating the absolute dates suggested by MT might well have been puzzled by the fact that Shem lived 500 years after the flood and died 35 years after his descendant Abram . . . . In order to correct this strange chronology, 100 years were added to the age given for Arpachshad to Serug at the birth of their first sons, plus 50 years to Nahor at this same milestone.”<sup>11</sup>

Also, the Alexandrian Jews who translated the LXX would have been familiar with Manetho’s history of Egypt,<sup>12</sup> which claimed the founding of Egypt was centuries earlier than the biblical date of the Flood. Stretching the Bible’s chronology with a simple, consistent change may have been an attempt to harmonize the two histories. As Larsson explains:

“According to this the first ‘historical’ pharaohs had lived almost 3,000 years earlier. Consequently there could not have been a flood over the whole world just 2,000 years earlier. The simplest way to avoid discussions and objections was to lengthen the time by adding another 100 years to the patriarchs’ ages when they begat their first sons. An extra generation (Cainan) also helped, which was incidentally a duplication of the following Shelah. By this process the total history was lengthened by 606 years before the flood and by 780 years after or in all almost 1,400 years.”<sup>13</sup>

As noted above, the LXX has an extra Cainan in the list. This is a well-known and unique feature of the LXX. Most scholars believe it was due to a simple copy mistake but it would also aid in the inflation of the LXX chronology.<sup>14</sup>

### Overcoming objections

There are some who believe the LXX preserves a superior text because the New Testament authors often quote from it. However, this is no different from an English-speaking pastor quoting from an English translation when he is preaching. The audience of the New Testament overwhelmingly spoke Greek and so it makes sense that the NT authors would use the Bible to which their audience had access. Furthermore, this paper does not address the overall merits of the LXX but specifically is looking at its text in these two chronogenealogies and linking passages. By standard text-critical analysis, these two *particular* passages are secondary when compared with the MT.

Does this mean that the Bible’s textual transmission is broken in some way? In fact, in many ways, the ‘democratization’ of transmission that resulted in so many variants actually aided the *preservation* of Scripture because



no one elite group could unilaterally change passages they did not like—there were simply too many copies. Over time, the accumulating variants mean that we come up with text families such as the MT, LXX, and SP, which can be weighed against each other. No text is always superior to the others (see discussion of Eber above for an instance where the MT was probably corrupted). However, using text-critical analysis, we can arrive at the probable original text by comparing all the variants.

Some would take exception to the assumption of inerrancy that has driven this analysis—for instance, we *assume* that any error, such as pre-Flood patriarchs living past the Flood, must be the result of a scribal error, rather than part of the original text. For instance, Hendel argues that the original genealogies were inserted into the narrative from another source with no thought of how things linked together.<sup>15</sup> However, his reconstruction is less parsimonious, requiring *all three* extant texts to be recensions of a flawed original. Instead, a single datum, the age of Jared when Enoch was born, appears to be an early gloss in the LXX/SP tradition that explains all the relevant chronological difficulties.

### Conclusion—the MT preserves a superior chronology

When one removes obvious inflations and clear textual errors, the MT, SP, and LXX are remarkably similar. This should give the biblical inerrantist confidence in the reliability of biblical chronology. All three texts agree that the antediluvian generations lived vastly longer than their post-Flood descendants (and the tendency was to *lengthen*, not shorten, these lifespans, at least for Genesis 11 LXX). All three agree that lifespans declined very quickly after the Flood, though Abraham, Isaac, and Jacob still lived substantially longer than modern people. And all three give a maximum age of the earth that is far less than 10,000 years. However, when we analyze the relatively small differences that do exist between the three versions, we come to the conclusion that the MT has the best claim for being closest to the original chronology penned by Moses.

We did not come into the analysis with the agenda of proving MT superiority. In fact, it was our intention to analyze the relevant details in a way to bridge the gap between several competing views. However after examining the relevant texts, the MT clearly has the superior claim to authenticity. Much of this work was presaged by Williams in his 1998 article, *Some Remarks Preliminary to a Biblical Chronology*, in this journal.<sup>16</sup> We have come to similar conclusions after including a few relevant points he did not mention but more work could be done. We encourage all parties to dig deeply into this matter and allow the data to point them in whatever direction they lead.

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12. See Bates, G., Egyptian chronology and the Bible—framing the issues; [creation.com/egypt-chronology](http://creation.com/egypt-chronology), 2014.
13. Larsson, G., The chronology of the Pentateuch, a comparison of the MT and LXX, *J. Bib. Lit.* 102(3):401–409, 1983; p. 402.
14. Pierce, L., Cainan in Luke 3:36—insight from Josephus, *J. Creation* 13(2):75–76, 1999.
15. “I have argued that the chronological problems of Genesis 5 and 11 are easily accounted for by the theory that a redactor incorporated a document, the סֵפֶר תּוֹלְדוֹת אָדָם [sēpher tōl’dōt ‘Adām] “Book of the Generations of Adam” into the preexisting text of Genesis without harmonizing the chronological data of the two documents. From there, we can discern clearly the chronological clashes that motivated the various scribal revisions.” Hendel, ref. 9, p. 78.
16. Williams, P., Some remarks preliminary to a biblical chronology, *J. Creation* 12(1):98–106, 1998; [creation.com/chronology](http://creation.com/chronology).

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# Nylon-eating bacteria—part 3: current theory on how the modified genes arose

Royal Truman

Since genes used by 'nylon-eating bacteria' surely arose subsequent to nylon manufacture, this has been argued as proof for evolution. In Part 3 of this series we interpret this phenomenon using Coded Information System Theory, emphasizing that change is not the same thing as random evolution. The nature and source of information-processing guidance producing useful change needs to be first understood to permit a rational discussion of the significance of biological novelty. We summarize here what is currently believed to lie behind modified amide-degrading genes and why the original frame-shift theory, refuted in Part 2 on the basis of data already available at the time it was published by Ohno, is no longer believed on the basis of new data.

In Part 1<sup>1</sup> and Part 2<sup>2</sup> of this series we discussed the phenomenon of degradation of waste products resulting from the production of nylon-6.<sup>3</sup> Since the responsible enzymes E-I – E-III in all likelihood arose, or at least were fine-tuned, after the introduction of nylon-6, this was used to argue no creator is necessary, by claiming novel proteins could arise by chance.<sup>4–6</sup>

A characteristic of information is that intention can be expressed during later periods of time and in other locations. The divine creation worldview presupposes that forethought, and front-loaded information, whether encoded on DNA or otherwise,<sup>7</sup> can explain the origin of novel features. Whether chance or design offers a better explanation for biological novelty should be easier to evaluate by understanding the mechanism by which it may have arisen and how it now works.

To illustrate, intron/exon splicing in eukaryotes generates a richer variety of valuable proteins than is possible for simpler prokaryotes. Chance or design? Only a tiny proportion of possible mRNA sequences are biologically useful, and correct intron/exon boundaries exist for hundreds of thousands of genes throughout nature. The potential for error is overwhelming. What could possibly drive the chance origin of such a scheme, which would be selected against again and again due to unsuitable outcomes? For the scheme to work, spliceosomes are needed *ab initio*, which are “composed of as many as 300 distinct proteins and five RNAs, making it among the most complex macromolecular machines”.<sup>8</sup> Evolutionary scenarios must be plausible if they are to be taken seriously.

We saw in Part 2 that initially virtually all scientists accepted unquestioningly Ohno's claim<sup>9</sup> that the enzymes had been produced by reading frame-shifts from pre-existing genes. No critical thought was given to whether this possibility would be more consistent with chance or design.

Dr Thwaites, a professor of biology at San Diego State University, wasted no time to gloat:

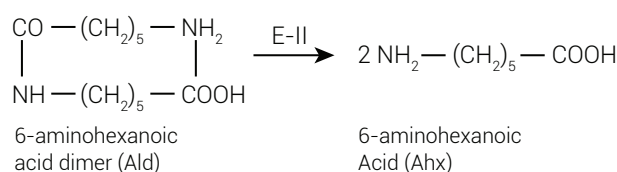
“We’ve been trying to explain all this to the protein ‘experts’ at ICR for the last seven years. We have told them that new proteins could indeed form from the random ordering of amino acids ... . Now it has happened! Not one, but two, new proteins have been discovered. In all probability new proteins are forming by this process all the time ... . DNA sequence suggests that a simple ‘frame-shift’ mutation could have brought about the chance formation of at least this one enzyme ... . All of this demonstrates that Yockey Hoyle and Wickramasinghe, the creationists, and others who should know better are dead wrong about the near-zero probability of new enzyme formation.”<sup>10</sup>

In Part 2 we showed how the storyline and debates based around Ohno's frame-shift theory and claim that genes arose from simple repetitive oligomers were formulated using evolutionary speculations masquerading as factual raw data.<sup>11</sup> Since most of the literature on the internet on the origin of E-I–E-III has not been removed or revised, anyone new to the subject is likely to believe the frame-shift mechanism is true.

In Part 2 we analyzed the reported data, already available at the time everyone accepted Ohno's notion, and this led to serious doubt he could have been right. Since then, new research, which we will discuss here, has led to universal rejection of Ohno's claim by the experts in the field. Incidentally, Dr Thwaites' triumphant statement, above, is factually wrong, both in terms of the frame-shift theory and probability of random peptide sequences producing a useful protein.

## Current belief about the origin of E-II

Aligning enzyme F-E-II (F for *Flavobacterium*) and F-E-II' sequences was reported to display 46 amino acid



enzyme E-II = 6-aminohecanoic acid oligomer hydrolase

**Figure 1.** Degradation of 6-aminohecanoic acid oligomer hydrolase (Ald) by enzyme E-II. Enzyme E-II = 6-aminohecanoic acid oligomer hydrolase.

alterations<sup>12,13</sup> after inserting some putative indels. The variant also present, F-E-II', had only 0.5% as much catalytic activity toward Ald (figure 1).

However, modifying only two amino acids in F-E-II' to match those found in F-E-II (G181 to D, and H266 to N) was enough to increase the Ald-hydrolytic activity up to 85% of the level of the putative parental F-E-II enzyme.<sup>14</sup> Alterations in the other 44 residues did not significantly increase the activity.

Negoro proposed that a common ancestral gene led to genes E-II and a variant E-II', found on plasmid pOAD2 of *Flavobacterium* sp. K172.<sup>13</sup> The authors were unable to produce good crystals of E-II' for crystallographic studies, so they modified five amino acids in E-II': T3A (i.e. Thr in position 3 was modified to Ala), P4R, T5S, S8Q, and D15G to match the residues found in E-II at these positions. The resulting gene, called *Hyb-24*, crystallized but displayed only the E-II' level of activity. It is unlikely these five amino acid substitutions, all within fifteen residues from the end of the protein, would distort the folded structure of E-II' significantly, so the crystallographic data should indeed reflect the folded structure of E-II' also quite well.

A single alteration in *Hyb-24*, G181D, increased the Ald-hydrolytic activity<sup>15</sup> by a factor of 11, and replacement of D (Aspartate) at position 181 in F-E-II with Asn, Glu, His, or Lys by site-directed mutagenesis drastically decreased the Ald-hydrolytic activity, but had little effect on the enzymatic activity of *p*-nitrophenylacetate (C2) and *p*-nitrophenylbutyrate (C4) esters.

The atomic coordinates of the deduced structure of *Hyb-24*, representing closely the protein product from E-II', was used with the DALI server<sup>16</sup> to find similar folded proteins stored in the Protein Data Bank.<sup>17</sup> The two-domain structure was found to be similar to the folds of the penicillin-recognizing family of serine-reactive hydrolases (which have a characteristic Ser-X-X-Lys motif),<sup>12</sup> especially to those of a d-alanyl-d-alanine-carboxypeptidase from *Streptomyces* (Z-score 26.7) and a carboxylesterase from *Burkholderia* (Z-score 24.1).<sup>18</sup> Even though high Z-scores were found, the amino acid identity with *Hyb-24* was very low, ranging from 10 to 19%.<sup>19</sup>

The E-II and *Hyb-24* enzymes possessed hydrolytic activity toward C2 and C4 esters, and based on the spatial

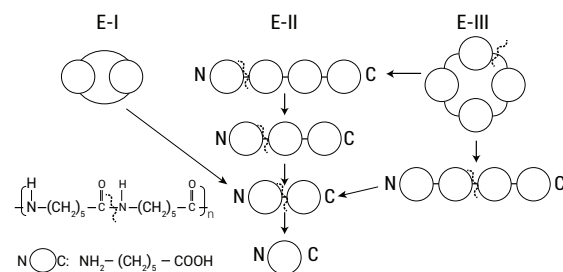
location and role of amino acid residues constituting the active sites for hydrolysis, the authors concluded that the ancestral gene was an esterase with a  $\beta$ -lactamase fold in which several amino acids were replaced in the catalytic cleft.<sup>20</sup> Subsequent, more detailed, crystallographic analysis on *Hyb-24* (PDB ID code: 1WYB) clarified the mode of catalysis down to the individual atom level and confirmed the mechanistic similarity with carboxylesterases. As further evidence, single substitutions of the key amino acids involved by site-directed mutagenesis led to the expected decrease in both nylon-oligomer and esterolytic hydrolysis, consistent with the three-dimensional model.<sup>21</sup>

The step-wise degradation process by the E-II enzyme (shown in figure 2) is very sensitive to structural details at the N-terminal part of the substrate.<sup>22</sup> Inappropriate binding in this region prevented it from degrading a large number of amides having various N-terminal residues. However, the enzyme was far less specific for various carboxyl esters, and weak hydrophobic interactions implied by the crystallographic data may contribute to the substrate binding.<sup>23</sup>

The data revealed convincingly how new activity towards nylon oligomer could easily arise with minimal changes while still retaining esterolytic functions.<sup>24</sup>  $\beta$ -lactamases can be structurally very different but the S-X-X-K motif is apparently necessary.

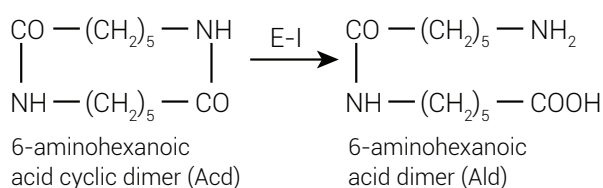
What remains unknown are the exact source of the precursor gene and the mutations which had occurred, but Negoro reiterated how changing only two residues in E-II' to match the amino acids found in E-II (Gly181 to Asp and His266 to Asn) increased the reactivity about 200-fold, to the level of E-II.<sup>25</sup> In addition, the other 44 amino acid substitutions played no role in the enzyme activity.<sup>26</sup> The same Shine-Dalgarno sequence was found in E-II and E-II', and the same position for the initiation and termination codons. This suggests the two shared a common ancestor, and, presumably, E-II could have easily arisen with just a few mutations from a suitable precursor.

In Part 1 of this series we mentioned that E-III genes were found in several kinds of bacteria. These were labelled *NylC<sub>p2</sub>* (from *Arthrobacter*), *NylC<sub>A</sub>* (from *Agromyces*) and *NylC<sub>K</sub>* (from *Kocuria*).<sup>27</sup> The polypeptides encoded have 355 residues in all three cases, the same ATG initiation codon, and the same Shine-Dalgarno sequences (GGAGG). *NylC<sub>A</sub>*



**Figure 2.** Biodegradation of 6-aminohecanoate-oligomer.





**Figure 3.** Degradation of 6-aminohexanoic acid dimer (Acid) by enzyme E-I.

and NylC<sub>K</sub> have 5 and 15 amino acid substitutions, relative to the NylC<sub>p2</sub> 355 residue sequence, but their genes are believed to reside on the chromosome and not plasmids.<sup>28–30</sup> These three enzymes are generated after a post-translational cleavage, which is a specific feature of the N-terminal nucleophile (N-tn) hydrolase family.

Four natural proteins very similar to Nyl<sub>A</sub> were found<sup>31</sup> using the DALI program. Crystallographic analysis and comparison with the enzymatic mechanism of other N-tn hydrolases suggested the key step for NylC relies on just four residues,<sup>32</sup> suitably held in place by the surrounding folded structure.

In *Pseudomonas* sp. NK87 the genes essential for the degradation of Acid (figure 3) were present on different plasmids. This implied that microorganisms were able to construct a sequential metabolic pathway of a synthetic xenobiotic compound by acquiring several plasmids encoding different enzymes. Later, these genes could be assembled into a single discrete unit through genetic rearrangements such as recombination and transposition.<sup>33,34</sup> Assuming this interpretation is correct, the whole process occurred in a suspiciously rapid manner, implying some kind of informational guidance.

The P-E-I (*Pseudomonas*) and F-E-I (*Flavobacterium*) genes, which degrade Acid, were 99% identical at the DNA level. The history of these genes has not been reported, and plasmids are perhaps transporting the mutated genes back and forth rapidly, providing selective opportunities. In strain K172 the two genes are located on the same plasmid, but in strain NK87 on separate plasmids. This suggests plasmid distribution of genes is important to permit degradation of synthetic substances.

The E-II gene of *Pseudomonas* sp. NK87 (P-E-II) and *Flavobacterium* sp. K172 (F-E-II) were found to have 53% sequence similarity and 35% amino acid sequence similarity (after inserting several putative gaps to optimize the alignment).<sup>5</sup> Another significant difference is that the codons used by the two enzyme variants for a key serine position was AGC in one case and TCG in the other, a difference of three single nucleotide mutations.<sup>35,36</sup> Unfortunately, the authors did not speculate about what the ancestral common gene may have been.

No similarity was found between the F-E-I and F-E-II enzymes, or between the F-E-I and P-E-II enzymes. This

implied the E-I and E-II enzymes arose independently,<sup>37</sup> and not via a gene duplication or a frame-shift mutation.

Negoro admits not knowing the molecular basis of nylon oligomer metabolism in strain PAO5502, but suggests that environmental stress favours this adaptation. He also provided a reference whereby micro-organisms may possess a cryptic gene which could be activated<sup>38</sup> (and perhaps optimized through a few mutations). Bacterial enzymes which would be improved by a single mutation will inevitably occur. The plasmid pOAD2 has 45,519 bp, and if the mutation rate would be about 1 mutation per 10<sup>10</sup> base pairs, typical of bacteria, then large populations of plasmid could already contain most acceptable single mutations, and there would also be many multiple mutational variants. Unlike chromosomal genes, plasmids need not necessarily be a permanent part of the bacteria, and damaged plasmids can be replaced by importing new ones or by carrying multiple copies. The tolerable mutational rate is likely to be higher than for chromosomal DNA.

## Discussion

### High mutation rates under stress

Micro-organisms were designed to be adaptable over a wide range of habitats and conditions. Adaptability includes fine-tuning by modifications of their DNA sequences. In the experiments described, various bacterial strains were subject to harsh conditions where survival would only be possible if a waste product from nylon production could be metabolized. Physiological details such as the availability of a given carbon source or other stress factors are known to affect mutation rate in bacteria, and so is the presence of transposable elements<sup>39</sup> (such as the *IS*6100 elements mentioned in Part 1), which can produce programmed re-combinations.<sup>40,41</sup>

Mutational hotspots are regions on chromosomes where mutations occur rapidly, and the mutability of a single base can vary by more than 10,000-fold.<sup>42</sup> Mutations need not be limited to reproduction, but also occurs in non-dividing cells, leading to the phenomenon of *adaptive mutation*, including the SOS mutagenic response, which involves more than SOS genes, associated with the protection, repair, replication, mutagenesis, and metabolism of DNA.<sup>43</sup>

Stress-induced mutagenesis can increase the mutation rate by several orders of magnitude under starvation conditions,<sup>44</sup> and is clearly a regulated phenomenon. The main cause is the use of error-prone DNA polymerases V (umuCD) and IV (dinB), which transiently increase the rate of mutation.<sup>40</sup> There are other forms for programmed DNA rearrangements, such as phase variation which is characterized by switching between high and low levels of activation of an ensemble of genes, which is also a tightly regulated process.<sup>40</sup>

Many bacterial populations include some members with a mutator phenotype. These bacteria can have a 10- to 50-fold increased mutation rate of up to 10,000 times, usually due to a defective methyl-directed mismatch repair system.<sup>36</sup> These variants tend to be less fit and the same stress conditions which trigger their generation seem to also initiate programmed cell death.<sup>45</sup> But nevertheless, under crisis conditions this subset could provide the means of generating a surviving new population.

## Conclusions

Negoro and others provided compelling evidence the enzymes involved in degrading the synthetic materials created during manufacture of nylon-6 were derived easily from existing precursors. The detailed steps were not identified, but it seems likely that the reaction being catalyzed is not very challenging, as Behe already pointed out,<sup>46</sup> and could be attained from many starting points and by many variants. The harsh nutritional challenges likely invoked pre-existing survival responses, which then led to increased mutations to survive at all costs.

Bacteria need to degrade and recycle organic substances into useful raw materials for themselves and other organisms. The huge population sizes, short generation times, robustness to a reasonable amount of mutations, and resultant ability to fine-tune general-purpose families of enzymes are part of the ecological design. If evolutionary principles really did lead to the vast complexity found in organisms, the examples produced as evidence must deal with the creation of complex proteins, molecular machines, organs and organisms, not merely their degradation into useful nutrients.

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# Bacterial genome decay from a baraminological viewpoint

Jean O'Micks

Bacterial genome decay (BGD) is common across bacteria, many aspects of which support the biblical creation/Fall model. The phenomenon can be traced through species comprising different baramins, with a common ancestor only a few thousand years old. Pseudogenization, genomic deletions, and the spread of insertion elements, chromosomal rearrangements, and genome downsizing are common, which are the opposite of what would supposedly happen during evolution.

We present a survey of the scientific literature describing BGD in the *Bordetella*, *Mycobacterium*, and *Yersinia* baramins plus their statistical genomic characterization. These baramins are contrasted with bacteria with highly reduced genomes and organelles. We also examine the consequences of BGD for the minimal organism question and the endosymbiotic theory. Based on a minimum gene estimate for the last universal common ancestor (LUCA) of 1,340, the probability for the evolution of the first non-parasitic cellular organism is approximately  $10^{-167,500}$ . Gene density, gene loss and the differences in genetic code separate organelles from bacteria with reduced genomes.

In conclusion, the study of BGD can be helpful in statistically characterizing baramins. It can delineate at what stage individual species are in this process within baramins. Genome size, gene number, and GC% can also help delineate individual baramins from one another.

Studying the decay of bacterial genomes is an interesting part of the creation/evolution debate. Certain aspects of bacterial genomes highlight natural processes that are more in line with the creation/devolution model compared to the evolutionary model of gradual upwards progression. The very fact that the scientific literature speaks about the genome decay in bacterial genomes strikes a massive blow to gradual upwards evolutionism and supports biblical creation, which states that genome decay is the result of the Curse.

First of all, bacterial genera (such as *Mycobacterium* or *Bordetella*) correspond to a large degree to the biblical baramins, or created kinds. Secondly, these taxonomical groups all have a common ancestor dating back only a few thousand years, which fits quite well within the biblical timescale. Thirdly, these bacterial genera also have undergone genetic bottlenecks in the recent past, along with other species, such as humans, during the Genesis Flood. Lastly, their genomes have undergone a process of decay, involving processes such as pseudogenization, deletions, spread of insertion elements, chromosomal rearrangements, and genome downsizing.<sup>1</sup>

For example, Wood<sup>2</sup> describes genome decay in the genomes of two *Mycoplasma* and *Ureaplasma* species. The 475 genes of *M. genitalium* are contained in the genome of *M. pneumonia*, with only a slight difference in gene order. However, only 53% of the genes in *Ureaplasma urealyticum* are found in either of the previous species. As genome decay progressed, these bacteria lost their genes and became more

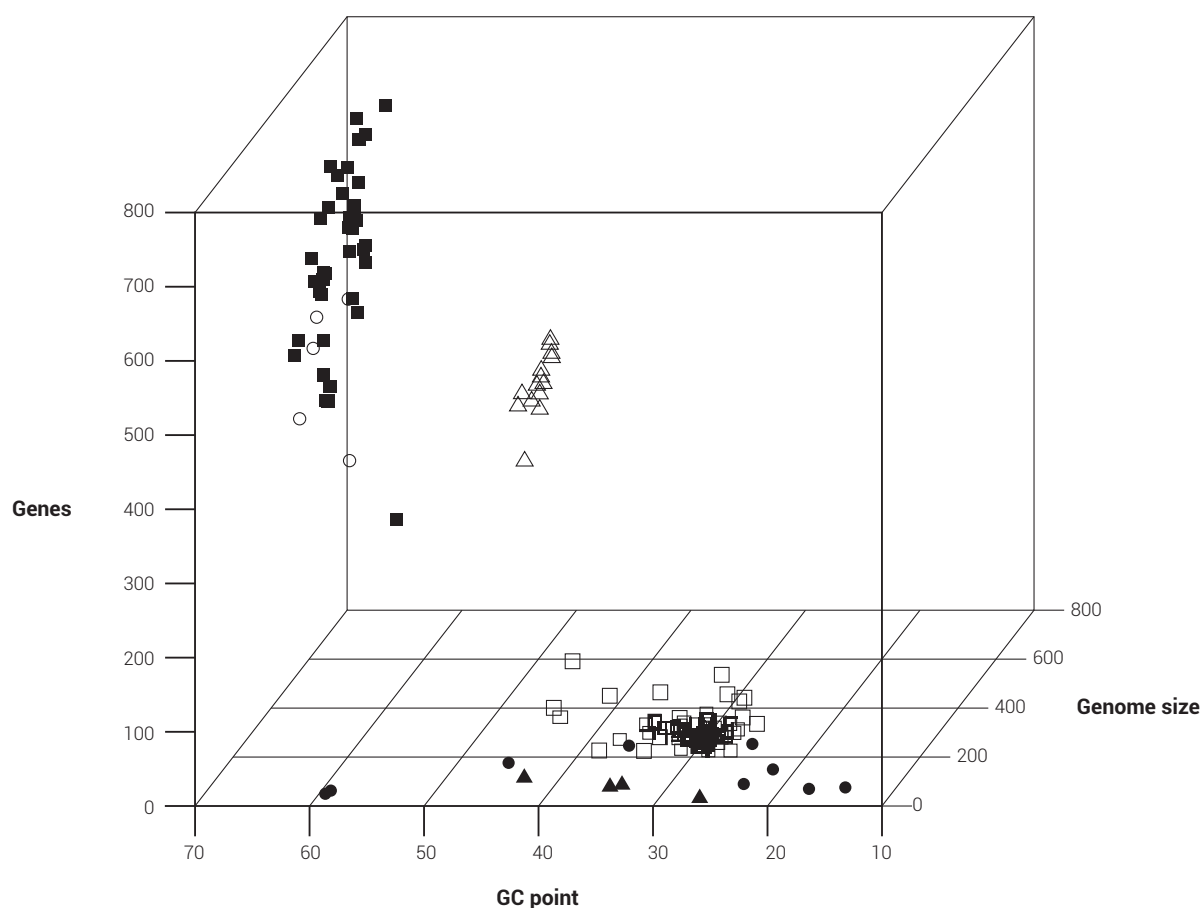
dependent on their hosts for survival (*M. genitalium* and *U. urealytica* are both found in the urinary tract of humans).

It is interesting to note that in these genera there are species, the genomes of which are in different stages of decay. This work describes these processes in a number of bacterial genera, such as *Mycobacterium*, *Bordetella*, and *Yersinia*. Some of the species in these genera cause illnesses such as leprosy, tuberculosis, Buruli ulcer, whooping cough, and the black plague. Related genetic phenomena, such as genetic entropy and the minimal genome, are also discussed from this aspect.

## The *Bordetella* baramin

A study by Parkhill *et al.*<sup>3</sup> examined three species of the *Bordetella* baramin: *B. bronchiseptica*, *B. pertussis*, and *B. parapertussis*, all of which colonize the respiratory tracts of animal species. *B. parapertussis* infects both sheep and humans, causing whooping cough in humans. Both species of bacteria have descended from the strains of the species *B. bronchiseptica*, which colonizes a broad range of hosts. During this process they underwent genome downsizing and changes in their virulence factors as well as changes in genes coding for enzymes in metabolic pathways. These species are thought to have originated from a common ancestor only a few thousand years ago due to lack of allelic polymorphisms.<sup>4</sup>





**Figure 1.** The number of genes as a function of genome size and GC%. Black square: *Mycobacterium* (40 data points), White circle: *Bordetella* (5 data points), White triangle: *Yersinia* (16 data points), White square: *Mycoplasma* (67 data points), Black circle: bacteria with reduced genomes (11 data points), Black triangle: organelles (4 data points).

In a study of 132 strains from these three species covering 32 different sequence types (ST), Diavatopoulos *et al.*<sup>5</sup> observed that *pertussis* and *parapertussis* have only appeared recently, implying that they descended from strains of *B. bronchiseptica*. From a bird's eye view, the genome sizes have decreased from the direction of *bronchiseptica* to *pertussis* and *parapertussis*. The number of coding sequences has decreased, whereas the number of pseudogenes has increased, a hallmark of genome decay. For exact numbers, see table 1,<sup>6</sup> where data is also given for the other groups. The genome sizes and number of genes for this as well as the other two baramins can be seen in figure 1. Here the *Bordetellae* baramin clearly separates from the other groups. Members of the *Mycobacterium* and *Bordetellae* baramin are intermingled with each other, but can be expected to separate from each other if more characteristics are taken into account besides such general ones like genome size or GC%. The correlation between the genome size and the number of genes in the *Bordetellae* baramin is 0.99.

Six hundred and two of the genes in *bronchiseptica* are unique to that species only. Besides this, there are several prophage sequences within the genome of *bronchiseptica* which were independently deleted—in spite of random chance—in the genomes of *pertussis* and *parapertussis*. This is evident because the edges of these prophage sequences are different in both species. The much smaller genome of *pertussis* is due to the widespread insertions of insertion sequence elements (ISE) (238 of them) into different parts of the *pertussis* genome, causing deletion and genomic rearrangements.

Many of the genes lost in the *pertussis* and *parapertussis* genomes are involved in utilization of alternative nutrient sources, such as autotransporter genes, some of which are involved in iron uptake, for example. Other genes include virulence factors, such as a type-IV pilus biosynthesis operon that is lacking from the other two genomes. Others include flagella, which are present in *bronchiseptica*, but not the other two species. This trend also exists in the *Yersinia*

baramin,<sup>7</sup> which will be described later. Finally, the genome of *bronchiseptica* contains a gene which codes for a type II-polysaccharide capsule, which contributes to survival in the environment.

In sum, in the *Bordetella* baramin the loss of genes due to genome decay is concomitant with the change in their pathogenicity. Loss of flagella or polysaccharides surface structures reduces the number of surface molecules which could be targeted by the human immune system. Herewith, the range of hosts is constricted as a byproduct of the process of genome decay. The resulting *Bordetella* species can hardly be candidates for evolution after losing so many genes in order to specialize to a tighter niche of a smaller number of host species.

### The *Mycobacterium* baramin

A similar process of genome decay has been observed in species of *Mycobacterium*. For example, *M. ulcerans*, a bacterium which causes skin lesions is prevalent in poor, rural areas and is transmitted by water insects. The *ulcerans* genome is regarded as an intermediate phase in genomic reduction towards the ultra-decayed *leprae* genome. Compared to the *marinum* genome, which is 6.6 Mbp coding for 5,426 genes, the *ulcerans* genome is 5.8 Mbp, and contains 4,160 CDs and 771 pseudogenes, with 1,064 Kbp of deletions compared to *marinum*,<sup>1</sup> and another 1,232 Kbp lost in *ulcerans* residing in 157 regions. However, a stretch of 475 Kbp was identified in *ulcerans* which is missing from *marinum*. These include sequences coming from the IS2404 and IS2606 insertion elements. The correlation between the genome size and the number of genes in the *Mycobacterium* baramin is 0.97.

According to a study involving 128,463 SNPs in the genomes of different *M. ulcerans* populations, it was shown by phylogenetic analysis that the *M. ulcerans* populations have all descended from a common *M. marinum* progenitor.<sup>8</sup> This involved the accumulation of insert sequences and pseudogenes, and large genome deletions which occurred in the *marinum* genome in its transition towards the *ulcerans* genome. These deletions took along with them genes involved in intermediary metabolism and respiration. It is within two distinct lineages of the *ulcerans* genomes that large-scale genomic rearrangements took place.<sup>9</sup> Pseudogenes accumulated in the *ulcerans* genome include *otsB* genes, involved in trehalose metabolism, and *gltA* genes, which are involved in glutamine synthesis. Another gene, *crtB*, which is involved in the production of light-responsive carotenoid pigments, which protect *marinum* from direct sunlight, has a corresponding non-functional ortholog in *ulcerans*, implying that it has to adapt to another more protected ecological niche, hindering it from evolution as in the case

of *B. pertussis* and *parapertussis*. The *marinum* genome has 192 CDs involved in substrate transport, whereas *ulcerans* has only 128. *Marinum* has more than 590 oxidoreductases, whereas *ulcerans* has more than 400. *Marinum* has 27 PKS genes in its genome, which are responsible for the production of secondary metabolites, whereas *ulcerans* has only 12. For example, the *cycdA* ortholog of the *cycdABCD* cytochrome is missing in *ulcerans*.<sup>1</sup>

Individual members of this baramin can be seen with members of the *Bordetella* baramin in figure 1.

Other species include *M. tuberculosis* and *M. leprae*, which cause tuberculosis and leprosy, respectively. Leprosy is a disease thought to have originated either in East Africa or India some 4,000 years ago, well within the biblical timescale.<sup>10</sup> Leprosy is still prevalent today, with reservoirs in Brazil and India, with 220,000 deaths reported in 2011. A most recent common ancestor of all extant and archaic *M. leprae* genomes existed some 1,400 to 2,700 years ago; *M. tuberculosis* is thought to have arisen from a cow pathogen, *M. bovis*, some 8,000–10,000 years ago. The *leprae* genome is much smaller compared to other *Mycobacterium* genomes (about 3.2 Mbp) and has a small number of active genes (~1,600), and a high number of pseudogenes (~1,300).<sup>11,12,13</sup> The *M. leprae* genome is so reduced, and it is has become so specialized, that the bacterium (an obligate parasite) can only be cultured in nine-banded armadillo. It grows so slowly in laboratory conditions that its cell division rate is 13 days. The bacterium has a propensity for infecting Schwann cells, and has lost three *Mce* operons encoding invasins, which are virulence factors.<sup>11</sup>

What makes the *M. leprae* genome interesting is its small genomic variance; leprosy genomes are >99.9% similar, and have only 807 polymorphic sites, and only 4–5 subtypes. They have found that ancient leprosy genomes are very similar to modern ones. Thus, due to this similarity if they can replicate factors and conditions that halted the spread of leprosy in the 14<sup>th</sup> century, then this could possibly put an end to the modern leprosy epidemic.<sup>14,15</sup> The *leprae* genome is very stable,<sup>16</sup> and is thus at the end stage of the genome reduction process.

### The *Yersinia* baramin

Bacteria such as *Yersinia pestis*, *pseudotuberculosis*, *fredericksonii*, *kristensenii*, *ruckeri*, and *enterocolitica* belong to the *Yersinia* baramin.<sup>17</sup> The bacterium *Y. pestis* is famous for causing three major pandemics throughout human history, the Justinian plague, the Black Death (bubonic plague), and the Chinese plague in the 19<sup>th</sup> century,<sup>18</sup> and has been classified into four biovars (Antiqua, Medievalis, Orientalis, and Pestoides), according to its spread.<sup>19</sup> Comparisons between four published genomes

**Table 2.** Different stages in bacterial genome reduction.

Stage	Characteristics	Typical genome size	Example species
Free-living stage	Few pseudogenes or mobile elements, stable genome	>1Mbp, >1,400 genes	<i>Prochlorococcus marinus</i>
Host-restricted pathogens	High number of pseudogenes, mobile elements, instable genome, reducing in size	<1Mbp, >500Kbp, >500 genes	<i>Mycobacterium ulcerans</i> , <i>leprae</i>
Endosymbionts	Highly reduced, stable genome, few pseudogenes or mobile elements	<500 Kbp, 200–500 genes	<i>Carsonella ruddii</i>

of *pseudotuberculosis* and of 133 *pestis* strains show that *pseudotuberculosis* is more variable, and that *pestis* developed only more recently.<sup>20,21</sup> During its descent from the ancestral *Yersinia* species, *Y. pestis* has undergone lateral gene transfer, pseudogenization of some 149 genes, spread of insertion elements, genome size reduction, and genome rearrangement.<sup>22</sup> Changes in the pathogenicity of *pestis* compared to *pseudotuberculosis* include genes involved in cell adhesion to the host gut, such as YadA and invasin, as well as gene coding for the flagellum and chemotaxis. *Y. enterocolitica* is motile in this respect.<sup>7</sup> Genes such as hmsT, iucD, or phoP involved in biofilm production, iron acquisition, or adaptation to the intracellular environment have also been implicated in gene loss.<sup>23</sup>

Members of the *Yersinia* baramin can also be seen to form a tight cluster by themselves in figure 1. This is due to their characteristically low GC% compared to the other three baramins. The correlation between the genome size and the number of genes in the *Yersinia* baramin is 0.97.

This divergence is estimated to have occurred approximately 6,500 years ago (nicely fitting into the biblical timescale), with little sequence diversity having accrued during this period.<sup>24,25</sup> This age might be as young as 1,500 years (with the Justinian plague in ad 541). The age can also possibly be set to 3,350 years, during the time of the prophet Samuel. 1 Sam. 6:4–19 describes a plague which was caused by mice as vectors in the land of the Philistines. Verse 4–5 state the following:

“Then said they, What shall be the trespass offering which we shall return to him? They answered, Five golden *emerods*, and five golden *mice*, according to the number of the lords of the Philistines: for one *plague* was on you all, and on your lords. Wherefore ye shall make images *of your emerods*, and *images of your mice that mar the land*; and ye shall give glory unto the God of Israel: peradventure he will lighten his hand from off you, and from off your gods, and from off your land.”

Here the emerods in the King James version are thought to be tumors, caused by the black plague. It was about this time that *Rattus rattus*, the black rat, which is the vector

for *Y. pestis*, arrived in the Middle East, and which are also interestingly noted in the passage from 1 Samuel. 1 Sam. 5:9 states: “And it was so, that, after they had carried it about, the hand of the LORD was against the city with a very great destruction: and he smote the men of the city, both small and great, and *they had emerods in their secret parts*.” Here the secret parts refer to the groin where plague tumors regularly broke out.

According to some interpretations of Revelation, the black plague could correspond to the first of the seven plagues, correlating the Bible with science and history: “And the first went, and poured out his vial upon the earth; and there fell a noisome and grievous sore upon the men which had the mark of the beast, and upon them which worshipped his image” (Rev. 16:2). Indeed, one of the characteristic symptoms of bubonic plague is the coloured sores which appear on victims’ skin.

### Trypanosomatids

Interestingly enough, the processes described in the previous bacterial baramins are also present in nearly all eukaryotic superkingdoms. This process includes pronounced genes loss, elimination of repetitive elements, and reduction of average intron sizes.<sup>26</sup> For example, the trypanosome *Trypanosoma cruzi*, a single-celled eukaryote and the etiologic agent of Chagas disease, has a genome of 60.3 Mbp, and an estimated 12,000 genes as well as 3,590 pseudogenes, which are a clear sign of genomic decay. About half of its genome is made up of repetitive sequences such as surface proteins, retrotransposons, and subtelomeric repeats. In comparison, *T. brucei* has a genome of 26.1 Mbp and only 8,800 non-redundant protein-coding genes and 500 pseudogenes. Its GC% is also smaller, 46.4%.<sup>27</sup> 103 long non-coding RNA (lncRNA) transcripts were shown not to have any protein-coding potential. While this makes up a substantial part of the pseudogenes in *T. brucei*, still a large number of pseudogenes remain which are truly functionless.

Some important genes which are either lost or have been pseudogenized include a photolyase homolog, and a number of endonucleases. The enzymatic machinery for



**Table 3.** Correlation between genome size, GC%, and gene number in different groups of bacteria and organelles.

	Genome size vs GC%	Genome size vs gene number	GC% vs gene number
<i>Mycobacterium</i>	0.43	0.97	0.41
<i>Bordetella</i>	0.55	0.99	0.51
<i>Yersinia</i>	-0.25	0.97	-0.28
<i>Mycoplasma</i>	-0.10	0.75	0.04
Bacteria with reduced genomes	-0.23	0.99	-0.27
Organelles	0.95	-0.54	-0.26

non-homologous end-joining is also seemingly missing. Homologs for genes such as MCM10, CDT1, DBF4, and CDC7 are missing. Important signaling molecules, such as serpentine receptors, heterotrimeric G proteins, as well as some PK genes are also missing. This gives the picture that trypanosomes are undergoing the process of genome reduction, similar to bacteria, hallmarked by the spread of repetitive elements and retrotransposons, and the loss of genes involved in DNA repair.<sup>28</sup>

### General genetic trends in bacterial genomes undergoing genomic decay

A description of the different stages in bacterial genome decay can be seen in table 2. From table 3 we can also confer that there is a very tight correlation with genome size and gene number. Besides gene loss, other trends are present in the genomes of bacteria. For example, recombination of genetic material occurs between closely related species, members of the same baramin. However, this does not count as production of new genetic material, as only existing genetic material is shifted, recycled, and repackaged. Horizontal gene transfer of plasmids and genes between species is also widely cited, but is in principle the same as recombination; no new genetic material is created during the process. Gene duplication is also cited for the creation of new genetic material. Gene duplication and divergence is not observable per se, as it is a process that requires the pseudogenization and sequential change of one copy of the duplicated gene into an entirely new gene.<sup>29</sup> However, we can completely disprove this notion by taking the following facts into consideration: it has been observed that two *strains* of the bacterium *E. coli*, that of K-12 and O157, differ from one another by 1.4 Mbp, which is one-quarter of its genome.<sup>30</sup> This means that roughly one fourth of the genes between these two strains would have disappeared due to this deletion. You could also think of this in an inverse manner: the O157 strain of *E. coli* has roughly 1,000 more genes (larger than the number of genes in the genomes of even some so-called minimal organisms, which we will discuss later) than the K-12 strain, yet they are both strains of the same species.

Gene duplication and divergence can only achieve this much! This situation is similar to that in plants, not just bacteria.<sup>31</sup>

Despite the glaring evidence for genome decay, a paper in the secular journal *Genome Research* states, “The loss of genes is not necessarily associated with the loss of DNA. In fact, the half-life of a pseudogene in some eukaryotic species may be hundreds of millions of years.”<sup>32</sup> Yet, according to Graur *et al.*, “it has been observed in bacteria that the tendency of these nonfunctional regions is to disappear from the genome in short periods of time [emphasis added]”.<sup>13</sup> So, observation of nature trumps secular religious beliefs. These observations come from a paper by Nilsson *et al.*<sup>33</sup>, which describe how methyl-directed DNA mismatch repair (MMR) protects chromosomal structure due to its antirecombinational activity. According to Nilsson:

“... sixty lineages were each serially passaged for 1,500 generations, and deletions, totaling 224,873 bp, were found in four of the lineages. From these numbers, we calculated the arithmetic mean DNA loss rate in the mutS lineages to be ~2.5 bp per chromosome per generation [i.e. 224,873 bp (total amount of DNA deleted) / (60 (number of lineages) x 60 (number of serial passages) x 25 (number of generations of growth per serial passage))].”

They assume that with a generation time of 1 day for a single bacterium, a genome with a functional MMR system can be reduced by 1 Mbp in 50,000 years, and without an MMR system in 1,000 years. The replication time of bacteria here is overstated; a study of *Bacillus* species<sup>34</sup> shows the replication time is more like 3 hours (8 times in a day), reducing the deletion time from 50,000 years to 6,250 years (8 times less) with an MMR, and to 125 years without one. These dates are within the biblical timescale.

### Genetic entropy in bacteria

What then will be the ultimate end of all this genome decay? If given enough time, bacterial genomes could erode so much that they would suffer a mutational meltdown. However, this is not so, as shown in a paper by Carter.<sup>35</sup> On the one hand, bacteria have smaller genomes and replicate

very quickly—a mutation or genomic decay would be felt very rapidly if bacteria didn't have very large population sizes and also lower mutation rates (around  $10^{-10}$  compared to  $10^{-6}$ – $10^{-8}$  in eukaryotes). Thus, if mutations did accrue, these bacteria would quickly be replenished by ones without the mutation.

Nevertheless, genetic entropy does accrue, due to the Curse, and even bacterial genomes decay to the point that some bacterial species are what is known as minimal organisms, the genomes and number of genes of which are both extremely small. The number of genes in minimal organisms is so small that they are just enough so that the organism is able to survive (again, the exact opposite of gradual, upwards evolution). Some exist outside the host cell, whereas others have become intracellular endosymbionts, such as *Rickettsia prowazekii*, the aphid endosymbiont *Buchnera aphidicola*, and the psyllid symbiont *Carsonella ruddii*, which holds the record for the smallest-sized genome ever, at just 160 Kbp.<sup>36,37</sup> Other endosymbiont bacteria colonize plant and fungal species as well.

### The minimal organism question

This is even more significant to the origins debate in that evolutionists must necessarily push for a minimal organism with as small a genome as possible. This is because if the number of genes is small enough, then it would be a lot easier for them to explain how a small number of genes were formed in the primordial chemical soup during abiogenesis.<sup>38,39</sup> Evolutionary theory here is at a definite disadvantage, because endosymbiont species are ruled out from the outset, since they must necessarily colonize larger organisms such as insects in order for them to survive (which weren't present in the chemical soup). As of yet, the smallest free-living genome that evolutionists could define is that of *Actionmarina minuta*, with approximately 800 genes and a genome size less than 1Mbp.<sup>40</sup> A minimal estimate for the gene content of the hypothetical/imaginary evolutionary superstar organism LUCA (last universal common ancestor) is around 1,340 genes.<sup>41</sup> This number was determined after analyzing 37,402 genes across 184 genomes, including genes from eukaryotic organisms with which to reflect LUCA's gene content most accurately.

This allows for a calculation of the probability of the first primordial cell arising from the chemical soup through random mutations. After looking at proteins from completed genomes representing one million sequences, scientists have been able to recognize 50,000 protein families; up from earlier estimates.<sup>42,43</sup> If we assume, conservatively speaking, that a protein has only 100 amino acids, then this means that the probability of a random sequence of 100 amino acids constituting a viable protein sequence is  $\frac{6 \cdot 10^4}{20^{100}} \approx 3.9 \cdot 10^{-126}$ .

However, if we need 1,340 proteins (the number of proteins in the genome of LUCA) to be available all at once, then *the probability is further reduced to  $\approx (3.9 \cdot 10^{-126})^{1,340} \approx 10^{-167,500}$* . This is the probability that a single-celled organism can arise from the chemical soup, and it is clearly unfeasible.

These bacteria themselves are generally cultivable only under laboratory conditions, or hardly at all. We know that besides evolutionists, there were no laboratories present during what is believed to be chemical evolution. In general, the smallest genome size of heterotrophic bacteria is around 1,300 genes; the minimum number of genes is still larger for free-living photoautotrophs, which code for more genes for the protein apparatus which transforms sunlight into energy. For example, *Prochlorococcus marinus*, the most abundant photosynthetic organism on Earth has around 1,700 genes. Many of these reduced genome non-endosymbiont bacterial species also depend upon the presence of other organisms to produce raw material that they themselves need for their metabolism.<sup>44</sup> These minimal organisms in themselves, by definition, constitute an irreducibly complex system, which is a hallmark of design and points to the existence of the supernatural Creator of the Bible. A good estimate of the minimum number of genes necessary for a stable single-celled organism would be between 1,400–1,500,<sup>39</sup> which is approximately the same number of genes which were estimated for LUCA. The minimal genome size for free-living bacteria is also around 1 Mbp.<sup>45</sup> In figure 1 we can see that there is a great gulf in the size of the genome and the number of genes between free-living bacteria and bacteria with reduced genomes, including endosymbiont species.

The case of endosymbiont bacteria is in itself noteworthy, since precisely due to endosymbiosis, genes unnecessary for living in intracellular are thus free to mutate, diverge, and differentiate as freely as possible, since all selection pressure has been relaxed on them. In other words, we have a scenario very much akin to the duplication of a great number of genes which are now free to mutate into newer genes. In this way we can test the 'duplication and divergence' hypothesis of evolution. Yet here in all cases the genomes of these endosymbiont bacteria we see genome reduction, loss of genes, pseudogenization, decrease in gene density, and the spread of transposons and other repetitive sequences. Even worse for evolution, Kuo *et al.*<sup>46</sup> hypothesize that the ratio of non-synonymous mutations to synonymous ones ( $d_N/d_S$ ) are consistently larger in organisms with smaller genomes. This also goes along with a general trend that A+T content also increases in genomes undergoing genomic reduction.<sup>47</sup> For example, there is a moderate correlation between genome size and GC% (which is the opposite of A+T content) in *Mycobacterium* (0.43) and *Bordetella* (0.55) and organelles (0.95), according to Table 3. This relation also

holds moderately to the relationship between GC% and gene number. Here the correlation is 0.51 for *Mycobacterium*, and 0.51 for *Bordetella*. This reflects mutational bias rather than adaptation through selection based on random mutations.<sup>48</sup> This is because if mutations were truly random, the A+T content in bacterial genomes would not change but stay roughly the same.

This AT mutational bias is universal in bacteria, and even in strict symbionts, as a high GC→AT transition ratio was measured in the endosymbiont species *Hodgkinia cicadicola*. Here 115 of 167 SNPs were shown to transition from GC to AT (68.9%).<sup>49</sup> The GC% of the genome of this organism is 58.4%, which is relatively high for endosymbionts. The mystery here for evolutionists is how could this species' genome have such a high GC% along with such a high AT mutation bias? An answer is made plausible according to creation science if this one species was created in a separate baramin which had high GC%.

### No help for the endosymbiotic theory

It turns out that many features of reduced bacterial genomes do not help the endosymbiotic theory. In the case of *Carsonella ruddii* we can see which genes count as being dispensable to a bacterial endosymbiont (and conversely, indispensable to free-living bacteria). Many genes involved in replication, transcription, and translation are lost. Histone-like and single-stranded proteins, gyrase is lost; 9 aminoacyl-tRNA synthetases and 15 out of 50 essential ribosomal components are lost. Furthermore, it has lost the capability of synthesizing three essential amino acids.<sup>35</sup> According to Bennett *et al.*<sup>50</sup>,

“... the propagation and establishment of obligate symbionts in successive host generations requires symbiont cell replication and division. However, this remains one of the major essential functions typically lost from bacterial symbionts with small genomes.”

This is remarkable, in that according to some evolutionary theories, the mitochondrion is derived from bacterial species which have undergone extremely massive genome reduction so as to result in organelles of eukaryotic cells. However, it is a well-known fact that mitochondria and chloroplasts divide and segregate within eukaryotic daughter cells.<sup>51</sup> This poses a problem for the endosymbiotic theory of evolution which states that organelles came from such endosymbiont bacteria with highly reduced genomes.

In general, the distribution of genes in bacterial genome is linear, with approximately one gene per Kbp of sequence. As we can see in table 3, the correlation between genome size and gene number is very significant, whereas for organelles, the correlation is moderately negative (-0.54). Insect symbionts

have retained core enzymes for chromosome replication, translation, and transcription, such as the replicative DNA polymerase *dnaE*, whereas in organelles, these genes have been lost.<sup>52</sup> However, the types of genes as well as the gene density are different in organellar genomes. For example, 90% of many plant mitochondrial genomes are noncoding,<sup>53</sup> and can vary in size from 300 Kbp to 2.9 Mbp in the mitochondria of *Cucurbitaceae*.<sup>54</sup> Even some viruses have extremely large genomes, such as Mimiviridae, with genomes over 1Mbp with over 1,000 genes.<sup>55</sup> Interestingly enough, these authors hypothesize that the common ancestor [the archebaramin] of the cucurbits had an unusually large mitochondrial genome which itself underwent genomic contraction. Add to this the fact that the ‘universal’ genetic code is not really universal; codons are differently assigned in a number of organellar genomes.<sup>56</sup> This is important to note, since if codons are re-assigned to different amino acids, this disrupts fluid evolution from one protein sequence to another through random base pair mutations. Genome expansion due to introns and repeat elements also occurs in chloroplast genomes, although to a lesser extent than mitochondrial genomes.<sup>57</sup> These considerations prove that mitochondrial genomes are much too different from the genomes of bacteria with reduced genomes. Therefore we cannot conclude that mitochondria arose from the reduction of such bacteria.

### Conclusion

Bacterial genome decay is a widespread phenomenon among different groups of bacteria whereby the size of the genome and the number of genes are continuously and starkly reduced. These groups of bacteria correspond to the created kinds of Genesis, and these genomic decay processes include pseudogenization, deletions, spread of insertion elements, non-random changes in base composition, and chromosomal rearrangements.

The species belonging to these created kinds have undergone genomic bottlenecks, and their common ancestor, in the case of a few of these created kinds examined in this review date back to only a few thousand years, consistent with the Bible. The process of genomic decay has also been observed in another major domain of life, in single-celled eukaryotes, and also does not necessarily need millions of years to occur. During this process many kinds of genes, involved in motility, metabolism, transcription, and replication are lost. From this, two things follow: a change in pathogenicity of the microorganism and a specialization to the host organism. High specialization due to gene loss makes it highly unlikely or impossible for the bacteria to be able to ‘evolve’ any further.



Further genome reduction in bacteria eventually leads to the minimal organism, which is defined as an organism which is capable of living freely in its environment without depending on a host organism for survival. Currently, the free-living bacterium with the smallest number of genes is *Actionmarina minuta*, with 800 genes. Advanced genome reduction leads to endosymbiosis with a host organism, where the bacteria receive nutrients and protection from the host in exchange for secondary metabolites or other nutrients. The minimal organism question is a great impediment for evolution, since it cannot explain how 800 fully functional genes arose through abiogenesis. Life does not come from non-life. This paper also presents a calculation for the possibility of abiogenesis to be  $10^{-167,500}$ .

The types of genes and gene density in organelles are different than those in bacteria. Organelle genomes also show signs of having undergone contractions, and also use different codons than do bacteria, which prove that organelles did not originate from bacteria. Since the differences in genome size and number of genes is so large between free-living and endosymbiont species, we can conclude that these are two major apobaramins, distinct from one another.

All in all, bacterial genomic decay goes counter to evolution, is a recent and fast-happening phenomenon, happening separately in different kinds of bacteria and other organisms, and is fully consistent with biblical creation.

## Materials and methods

The data points depicted on figure 1, and also listed in table 1,<sup>6</sup> were taken from McCutcheon, 2011 and [www.ncbi.nlm.nih.gov/genome](http://www.ncbi.nlm.nih.gov/genome). Here genome size, GC%, the number of genes, and the number of pseudogenes were from the representative genome information for each species from NCBI. Only those species were analyzed which had complete data. A data frame for R was made by creating a txt file with the genome size, GC%, and gene number for each species as well as a number denoting which group the species belonged to (*Bordetella*, *Mycoplasma*, *Yersinia*, or bacteria with reduced genomes, organelles).

Figure 1 was generated with the scatterplot3d command using R version 3.1.0. The following commands were used:

```
library("scatterplot3d")
pch=c(0,1,2,15,16,17)
bgd<-read.table("BGDdata.txt",header=T)
scatterplot3d(bgd[,1:3], pch=bgd[,4], angle=240)
```

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# Did Darwin plagiarize Patrick Matthew?

Dominic Statham

There can be no doubt that Patrick Matthew preceded Darwin in articulating the theory of evolution by natural selection. Darwin claimed that he knew nothing of Matthew's work prior to publishing the *Origin of Species*. Some doubt this, arguing that in places his early writings appear too similar to Matthew's to be explained by coincidence. The book in which Matthew documented his theory was well known among naturalists and it would seem unlikely that Darwin would not have read it.

In 1831, the Scottish laird Patrick Matthew (1790–1874; figure 1)<sup>1,2</sup> published a substantial work titled *On Naval Timber and Arboriculture* (NTA).<sup>3</sup> Its primary subject was how to grow trees so as to provide Britain's warships with the best quality timber. As the owner and manager of a large orchard, Matthew had extensive experience of husbandry and breeding. This led him to speculate about what he termed 'the natural process of selection' and how it could have driven changes in plants and animals over long periods of time. Following the French naturalist Georges Cuvier, Matthew believed in an ancient Earth which, during the course of its long history, had been subject to periodic catastrophes—great floods that had wiped out many plants and animals across the earth. In Matthew's thinking, after each catastrophe, new types of organisms had arisen, as the creatures that survived the floods spread out into the newly created environments. This, he thought, explained why the different rock layers contain different fossils.

Matthew's treatise included the two pillars of what became known as Darwin's theory of evolution: variation and selection. Of variation, he wrote that it is "one of the most evident traits of natural history, that vegetables as well as animals are generally liable to an almost unlimited diversification"<sup>4</sup>, and of selection:

"There is a law universal in nature, tending to render every reproductive being the best possibly suited to its condition ... to their highest perfection, and to continue them so. This law sustains the lion in his strength, the hare in her swiftness, and the fox in his wiles ... those individuals who possess not the requisite strength, swiftness, hardihood, or cunning, fall prematurely without reproducing—either a prey to their natural devourers, or sinking under disease ... their place being occupied by the more perfect of their own kind, who are pressing on the means of subsistence."<sup>5</sup>

Unambiguously anticipating Darwin, Matthew wrote of the "circumstance-adaptive law, operating upon the slight but continued natural disposition to sport [i.e. produce variation] in the progeny".<sup>6</sup>

Richard Dawkins, keen to protect Darwin's reputation, claimed, "Matthew seems to have seen selection as a purely

negative, weeding-out force".<sup>7</sup> This, however, is clearly wrong. For example, Matthew wrote of how "the progeny of the same parents, under great difference of circumstance, might, in several generations, even become distinct species, incapable of co-reproduction."<sup>8</sup>

On reading of Darwin's *Origin of Species*, Matthew wrote to the *Gardeners' Chronicle*, asserting his priority to the theory of evolution by natural selection in no uncertain terms:

"In your Number of March 3rd I observe a long quotation from the *Times*, stating that Mr. Darwin 'professes to have discovered the existence and *modus operandi* of the natural law of selection', that is, 'the power in nature which takes the place of man and performs a selection, *sua sponte*', in organic life. This discovery recently published as 'the results of 20 years' investigation and reflection' by Mr. Darwin turns out to be what I published very fully and brought to apply practically to forestry in my work 'Naval Timber and Arboriculture', published as far back as January 1, 1831 ..."<sup>9</sup>

Darwin's reply appeared in the same magazine a fortnight later:

"I freely acknowledge that Mr. Matthew has anticipated by many years the explanation which I have offered of the origin of species, under the name of natural selection. I think that no one will feel surprised that neither I, nor apparently any other naturalist, had heard of Mr. Matthew's views, considering how briefly they are given, and that they appeared in the appendix to a work on Naval Timber and Arboriculture. I can do no more than offer my apologies to Mr. Matthew for my entire ignorance of his publication. If another edition of my work is called for, I will insert a notice to the foregoing effect."<sup>10</sup>

This he did in the third edition of the *Origin of Species*:

"In 1831 Mr Patrick Matthew published his work on 'Naval Timber and Arboriculture', in which he gives precisely the same view on the origin of species as that ... propounded by Mr Wallace and myself ..."<sup>11</sup>



### A plausible excuse?

Some scholars have questioned Darwin's honesty in making the claim that he had not heard of Matthew's views.<sup>12</sup> Moreover, it is difficult to take seriously the opinion expressed in Wikipedia, that "there is no evidence whatsoever that Darwin had read the book".<sup>13</sup> Loren Eiseley, formerly Professor of the History of Science at the University of Pennsylvania, argued that Darwin clearly drew upon *NTA* in essays he wrote in 1842 and 1844.<sup>14</sup> For example, Matthew refers to the 'natural process of selection'; Darwin refers to the 'natural means of selection'. In *NTA*, Matthew observes that under domestication, due to man's interfering with this 'natural process of selection', greater varieties of plants have arisen:

"Man's interference, by preventing this natural process of selection among plants, independent of the wider range of circumstances to which he introduces them, has increased the difference in varieties, particularly in the more domesticated kinds ..."<sup>15</sup>

In his 1842 essay, referring specifically to arboriculture, Darwin makes exactly the same point:

"In the case of forest trees raised in nurseries, which vary more than the same trees do in their aboriginal forests, the cause would seem to lie in their not having to struggle against other trees and weeds, which in their natural state doubtless would limit the conditions of their existence."<sup>16</sup>

Another example is Darwin's apparent regurgitating of Matthew's law of "adaptation to condition"<sup>17</sup> leading to a general uniformity within species. In *NTA* Matthew wrote:

"... a considerable uniformity of figure, colour, and character, is induced, constituting species; the breed gradually acquiring the very best possible *adaptation* of these *to its condition* [emphasis added] ..."<sup>18</sup>

Similarly, in his 1844 essay Darwin argued,

"How incomparably 'truer' [i.e. more uniform] then would a race [be] produced by the above rigid, steady, natural means of selection, excellently trained and perfectly *adapted to its conditions* [emphasis added] ..."<sup>19</sup>

Yet another example is Darwin's reference to 'long-continued selection',<sup>20</sup> the exact same phrase used by Matthew in *NTA*.<sup>21</sup> Darwin may, however, have read this same phrase in a book by David Low on plant cultivation and animal husbandry.<sup>22</sup>

Hugh Dower also makes a case for Darwin having read Matthew before publishing the *Origin of Species* in 1859.<sup>23</sup> A review of *NTA* appeared in the 1832 edition of *The Gardener's Magazine*,<sup>24</sup> which mentioned Matthew's views on "the origin of species and varieties". Darwin had clearly read this edition as he referred to it in a letter<sup>25</sup> and in a footnote on p. 69 of his *Natural Selection* manuscript,<sup>26</sup> both of which

were penned prior to 1859. Volume 3 of John Loudon's legendary *Trees and Shrubs of Britain* (1838)<sup>27</sup> refers to Matthew and *NTA* nine times. Since Darwin cites this very volume twice in *Natural Selection* it would seem most unlikely that he had not read these passages—particularly as, in one case, the page he refers to (p. 1374) is so close to one which quotes Matthew (p. 1380).

Matthew's letter to the *Gardeners' Chronicle* claiming priority for the theory of evolution was published on 7 April 1860. Three days later, on the 10<sup>th</sup>, Darwin penned a letter to Charles Lyell in which he discusses Matthew's letter and states that he had ordered a copy of *NTA*;<sup>28</sup> then, three days after that, on the 13<sup>th</sup>, Darwin wrote to Joseph Hooker making clear that he had read it.<sup>29</sup> Dower remarks that it seems unlikely that Darwin, living in the 19<sup>th</sup> century, and at home in Downe over Easter, would have obtained and read the book within just six days. Dower considers it more likely that Darwin, in fact, already had a copy.

### An obscure writer?

Darwin's reference to Matthew as "an obscure writer on forest trees"<sup>30</sup> and his suggestion that, perhaps, no other naturalist knew of Matthew's work<sup>10</sup> appear hollow in

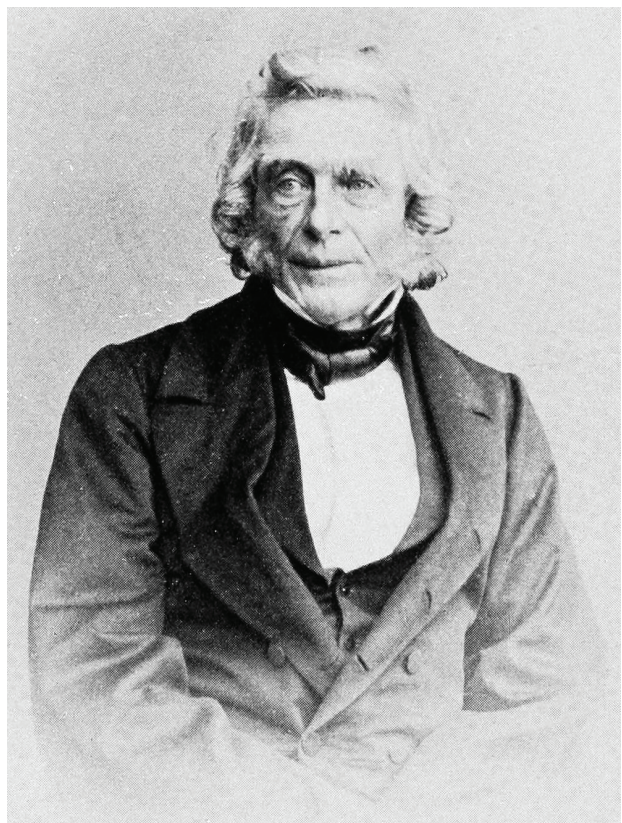


Fig. 1. Patrick Matthew (1790–1874).

the light of the facts. Matthew owned the largest orchard in Scotland and his work was quoted by researchers not only in Scotland and England but also the USA and India. Moreover, he was clearly known to a number of prominent naturalists as they actually cited his work. These included John Loudon, Prideaux John Selby, and Cuthbert Johnson. Loudon was a towering figure in the world of 19<sup>th</sup>-century botany, publishing, among others, *The Encyclopaedia of Agriculture*, the *Gardener's Magazine*, the *Magazine of Natural History*, and his *magnum opus*, *Trees and Shrubs of Britain*. He was likely well acquainted with *NTA* as it was his *Gardener's Magazine* that had published the review mentioning its dealing with “the origin of species and varieties”.<sup>24</sup> He had probably also given some thought to natural selection as Edward Blyth had published his papers on this subject in Loudon's *Magazine of Natural History*.<sup>31–33</sup> Selby was another renowned 19<sup>th</sup>-century naturalist who was well acquainted with Matthew, citing him numerous times in his *History of British Forest Trees* and referring to *NTA* as “a valuable treatise on Naval Timber”.<sup>34</sup> Selby also edited Alfred Russel Wallace's 1855 paper on evolution, written while Wallace was in Sarawak, Borneo.<sup>35</sup>

Indeed, Darwin's contention that probably no other naturalists knew of Matthew and his views utterly crumbles in light of even a moderate amount of research. An advertisement for *NTA*, taking up more than half a page, can be found in the opening pages of volume 4 of the seventh edition of *Encyclopaedia Britannica*, published in 1832 (figure 2). Matthew's book would have seemed essential reading for Darwin as the advertisement made clear that “the interesting subject of Species and Variety is considered ... and the causes of the variation ... pointed out”. Volume 21 of the same edition also cites Matthew and describes *NTA* as “a work which abounds in much sound practical information”. Although the 17<sup>th</sup> edition of *Encyclopaedia Britannica* is known as the ‘1842 edition’ it was published in stages between March 1830 and January 1842, making the contents available to Darwin before he wrote his 1842 essay in June of that year.<sup>36</sup> Large advertisements for *NTA* were also placed in *Quarterly Literary Advertiser* (January and November 1831) that again mentioned “the interesting subject of Species and Variety”. Advertisements and reviews also appeared in many other publications.<sup>37</sup>

7

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Fig. 2. Advertisement for *NTA* placed in volume 4 of the seventh edition of *Encyclopaedia Britannica* (1832).

## An obscure publication?

Using a method he refers to as “Internet Date-Detection” or the “ID Research Method”, criminologist Dr Mike Sutton provides strong evidence that *NTA* was, in fact, widely read.<sup>38</sup> Many 18<sup>th</sup>- and 19<sup>th</sup>-century books have now been scanned and can be Google searched using a date filter. This enables researches to discover who first used—and therefore probably originated—certain phrases. For example, using this method, Sutton demonstrated that Patrick Matthew was the first to coin the phrases ‘natural process of selection’, ‘long continued selection’, ‘admixture of species’, ‘threatened ascendancy’, ‘sport in infinite varieties’, ‘adapted to prosper’, ‘greater power of occupancy’, ‘power to permeate’, and many more. What is significant, however, is that many of Matthew's original phrases appear in literature written soon after he first penned them. For example, in 1834, Conrad apparently reproduced Matthew's phrase ‘admixture of species’; in the same year, Low referred to ‘long continued selection’; in 1837, Wilson wrote about ‘threatened ascendancy’; in 1841, Johnson used the phrase ‘adapted to prosper’; and in 1842, Selby used ‘greater power of occupancy’.<sup>39</sup> Remarkably, Robert Chambers, in his review of the first edition of the *Origin of Species*, used Matthew's phrase, ‘natural process



of selection' rather than Darwin's phrase 'process of natural selection'.<sup>40</sup> Chambers was the author of the infamous 1844 pro-evolutionary treatise *Vestiges of Creation*, and must have known of *NTA* because it was cited in a journal he had edited in 1832.<sup>41</sup>

Darwin's excuse that Matthew's theory of evolution appeared only "in the appendix to a work on Naval Timber and Arboriculture" also seems lame. Matthew referred to both variation and selection in the main part of his book as well as in the appendix, examples being his reference to plants and animals as "generally liable to an almost unlimited diversification" (p. 106), the principle of 'greater power of occupancy' (p. 302), and the term 'natural process of selection' (p. 308). Moreover, a work on arboriculture would have been of great interest to Darwin, especially one dealing with fruit trees. The first sentence of Darwin's first notebook on evolution<sup>42</sup> refers to these, and later, in the same notebook, he mentions crab apples and specifically the Golden Pippin, a variety which Matthew grew in his orchard. Again, twenty pages later, Darwin refers to a discussion of Pippin trees with William Fox. Interestingly, Matthew had written about these in a letter published in *Memoirs of the Caledonian Horticultural Society*, a magazine that Darwin had very likely read as it appears in his 'Books to be Read' notebook.<sup>43</sup>

### An unnoticed work?

Darwin's claim that he had never heard of *NTA* stretches credibility a long way. Before publishing the *Origin of Species*, he had spent over 20 years searching for every scrap of information he could find about species, varieties, and breeding. He moved in privileged circles, had a very wide correspondence and knew many leading naturalists. Selby, who was very familiar with *NTA*, and had edited Wallace's papers on evolution, was a fellow member of the Linnean Society. Chambers, who may well have known Matthew,<sup>44</sup> and whose *Edinburgh Journal* referred to him on two occasions,<sup>41,45</sup> was a fellow member of the Geological Society of London and was clearly acquainted with Darwin as they engaged in correspondence.<sup>46</sup> In fact, Chambers even gave him a copy of his *Vestiges of Creation*.<sup>47</sup>

Whereas in the UK today there are hundreds of publishers of scientific literature, in the 19<sup>th</sup> century there were very few, and they comprised a much more tightly-knit community. For example, Chambers, a publisher himself, would certainly have known Adam Black, the publisher of *NTA*, as they were both Scots and Fellows of the Royal Society of Edinburgh—along with Selby. John Murray, the company that published the *Origin of Species*, also published the *Quarterly Review*, which had, in 1833, included an article that discussed Matthew and *NTA*.<sup>48</sup> The father of Joseph Hooker, a close

friend of Darwin, had one of his books reviewed in the same volume which contained Loudon's review of *NTA*.<sup>49</sup>

Of those associated with Darwin's social network and who definitely read *NTA*, Selby was probably the best connected. Sutton comments:

"[Selby was] closely associated with William Hooker, Charles Lyell, Thomas Huxley and, most importantly, with Darwin by way of their mutual senior capacities at the British Association for the Advancement of Science and the Linnean Society. Selby was a very close friend of Darwin's great friend Leonard Jenyns ... . Jenyns wrote a book about Selby in which he recorded visiting him at his home along with none other than Darwin's father. Given Selby's obvious enthusiasm for *NTA*, his interest in Matthew's natural selection concept of 'greater power of occupancy' and his obvious respect for its author's knowledge of arboriculture, it seems highly unlikely that he would not have discussed *NTA* at the very least with other connected gentlemen of science. For this scientists get together and establish such societies, associations, clubs, committees and standing conferences, and it was at these gatherings where Selby mixed with both Darwin and Darwin's closest friends, many of whom Jackson reveals were his house guests."<sup>50</sup>

In the light of this well-documented evidence, is it really plausible that nobody had drawn Darwin's attention to Matthew's well-publicized, well-read book, which dealt specifically with the very subject Darwin was so well-known for studying? It has been argued that, had Darwin known of Matthew, some incriminating evidence would have been found in his now fully searchable correspondence. However, other very significant letters have mysteriously gone missing, such as those Darwin received from Alfred Wallace over a three-year period. Wallace researcher Dr Barbara Beddall considered this "very odd" and concluded that someone had "cleaned up the file".<sup>51</sup>

### Darwin—the perfect gentleman?

A number of commentators have drawn attention to Darwin's apparent unwillingness to credit others when he built on their work. Samuel Butler, for example, one of Darwin's contemporaries, accused him of passing over Buffon, Lamarck, and even his own grandfather, Erasmus.<sup>52</sup> Eiseley makes a good case for Darwin not only plagiarizing Matthew, but also drawing substantially from Edward Blyth in his 1844 essay and the *Origin of Species*.<sup>53</sup> Yet, although Darwin mentioned Blyth on a number of occasions, he did not cite his papers on natural selection even though he unquestionably knew of them. Similarly, Eiseley argued that he drew from Carl Vogt in writing *The Descent of Man*.<sup>52</sup> Darwin biographer Ronald Clark also recognized



the likelihood of Darwin having read *NTA*, opining, “Only the transparent honesty of Darwin’s character ... makes it possible to believe that by the 1850s he had no recollection of Matthew’s work.”<sup>54</sup> Others, however, might consider the weight of evidence against him to be just too strong.

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# Creation, the Trinity, and the emperor without clothes

Ian Hodge

This essay applies the concepts of God, the Trinity, and knowledge, from my previous article, into a powerful apologetic that can be used against the unbeliever. The unbeliever presents the view that the universe is uncreated, or undesigned. But such a view makes knowledge impossible.

In my essay, *Trinity's Truth Confirmed in Creation*,<sup>1</sup> I provided a way of looking at God as Triune that involved the questions of epistemology. In particular, the breakdown of knowledge from particulars to universals. It is the Christian view of God as Trinity that provides an explanation for the origin of the knowledge questions concerning the relationship of the one-and-many. Christian theism thus provides a framework for the development of knowledge and it is not surprising to find why science has developed where Christianity has flourished.

In this essay, I wish to explore the implications of those ideas in practical Christian apologetics. For the doctrine of the Trinity, far from being an abstract doctrine, provides a fundamental foundation in how the world is viewed.

In 2 Corinthians 10:5 we read: "We destroy arguments and every lofty opinion raised against the knowledge of God, and take every thought captive to obey Christ." This is Paul's claim of what he was doing and we are encouraged to do the same, to destroy arguments raised against the knowledge of God. In this essay, I want to show how it is possible to completely undermine the unbeliever's worldview.

In one sense, the arguments presented in this paper are 'logically prior to' the arguments in my earlier essay. If the unbeliever cannot get off the ground in differentiating between one object and another, then he does not need universals to help explain the particulars. Thus, I want to strip unbelief to its bare essentials, then show that the unbelieving self-proclaimed emperor has no clothes.

## A Christian philosophy of 'facts'

Basic to the unbeliever's worldview is a denial of creation—the ordered arrangement of the universe according to the mind of God. It is essential in Christian theism that we hold to the idea of an ordered universe in such a way that we can present the 'facts' of the universe as ultimately being tied together in the mind of God. The role of human endeavour, in the dominion mandate (Genesis 1:26), is to uncover these

relationships and use them to better the human condition. Robert Reymond explains this issue well:

"God created the universe, and has continually governed it according to His plan. Every fact in the universe is what it is, therefore, by virtue of God's prior knowledge. Every fact in the universe has meaning by virtue of its place in the unifying plan of God. No fact in the universe exists independently of God. *There is not one non-theistic fact in the universe.* Even the most insignificant single fact reveals God as its Creator as truly as the most obvious one does. Man himself, physically, rationally, reveals God. If one wonders how it is that the God of Christian theism has interpreted every fact of the universe, that is, how it is that He has placed a meaning on them I would reply, first, *by the creative act itself.* He has interpreted this fact a 'star' by creative fiat. He interpreted that fact a 'bird' by created act. Second by *subsequent special revelation.* He created light and 'called' it day (Gen.1:5). He created an expanse and 'called' it heaven (Gen. 1:8). ... It would follow then that if a man learns a fact to any degree, his knowledge of that fact to the degree he knows it at all, has to be in accord with the prior divine interpretation of it. ... In other words, the word of the God of Scripture is the final and ultimate 'court of appeal' in every area of human existence. It is only on the basis of the Christian faith alone that man can justify knowledge at all [emphasis in original]."<sup>2</sup>

The alternative to an ordered universe is an unordered universe. Carl Sagan posed the question as to whether the universe was cosmos or chaos.<sup>3</sup> There is no middle ground here.

Sagan's question allows us to present not just a philosophy of science in general but a philosophy of factuality in particular. As already stated, the Christian philosophy of factuality is that all the facts of the universe are tied together in the mind of God. There is not one single piece of the created order that is not where it is, at the time it is, and the



Figure 1. What is this?

size that it is, that is not the result of God's ultimate plan for His creation. Only on this basis is there a genuine *universe*.<sup>4</sup>

In my earlier article, I argued that knowledge requires the ability to differentiate between individual objects. This is done by means of universals, or what we might call categories. Examples of categories would be horse, chair, dog, cat, plants, animals, and so forth. Now in the Christian scheme of things, categories, or universals, were a part of the creation act of God. In other words, they are not man-made categories. You just need to remember one thing: without universals there is no knowledge of particulars.<sup>5</sup>

Let's argue, for a moment, that the unbeliever's worldview is somehow a true picture of the universe, that it is uncreated, unordered, and therefore chaos. Another way of saying this is that the facts of the universe are not where they are by design, but by chance, or some notion of random activity.<sup>6</sup>

Now here we come to a remarkable issue that can be easily overlooked. *Random facts cannot be known*. They are what the philosophers call *brute facts* and a brute fact is one that cannot be identified or explained.<sup>7</sup> This is a question of logic that flows over into our philosophy of science, so it becomes a question of science as well.

The issue, then, is this: is it possible to have science if the facts of the universe are unordered, that is, they are random? Consider figure 1. What do you see? If you say you see a white line on a black background, you have already *assumed* there is some connection of the facts with each other. In this case, your observation of a white line is, firstly, connected to colour and, secondly, connected to geometry. But in the unbeliever's universe of chance, no such connections can be identified or explained.

Now this notion seems so very strange to us today. But that is because we are so used to thinking of the universe as an *ordered* arrangement of facts and we find it difficult to comprehend the alternative. Because of our Christian worldview heritage, we are so comfortable with the notion

of arranged and ordered facts that we probably never stop to consider the alternative.

If the unbeliever's worldview is correct, however, everything that comes into existence does not come with relationships to other facts. Every item is unique. But if it is so unique that it has no connections, then science becomes an impossible project. Thus, the words of molecular biologist, Gunther Stent:

"The scientist thinks he recognizes some common denominator, structure, in an ensemble of events, infers these events to be related, and then attempts to derive a 'law' explaining the cause of their relation. An event that is unique, or at least that aspect of an event which makes it unique, cannot therefore be the subject of scientific investigation. For an ensemble of unique events *has* no common denominator, and there is nothing in it to explain; such events are *random*, and the observer perceives them as noise [emphasis in original]."<sup>8</sup>

### Why science is impossible on the assumption of atheism

This is really important to grasp. If what the unbeliever says about the origin of the universe were true, then science is dead in the water. Imagine the first human in the unbeliever's view. He knows nothing. He has no 'science' to work with. He has to start the whole endeavour of knowledge from scratch. But he has no laws, no 'common denominators' that he can use. So he picks up his first piece of the universe, or observes it in some manner, and now what will he do with it? What *can* he do with it? Very little. Again the words of Reymond:

"The universe is a compound of an overwhelming number of particulars. (Everything in the universe is viewed by the philosopher as a particular.) If every particular a man encountered (and remember the man himself is a particular composed of particulars) remained for him unique and completely unclassified and unclassifiable ... knowledge and communication would be impossible, for nothing would have meaning."<sup>9</sup>

In the unbeliever's worldview, the universe is merely a vast puzzle. Do the pieces fit together in some fashion? He does not know. And even if he thought they did fit together, where does he place the first piece of the puzzle? Does he have it in the correct place? How would he know?

Imagine you're sitting in front of a 10,000-piece jigsaw puzzle that has no interlocking edges. There is no finished picture of what the puzzle is supposed to look like once it is assembled. The edges cannot guide you to identify how one piece connects to another. Maybe colour can help you,

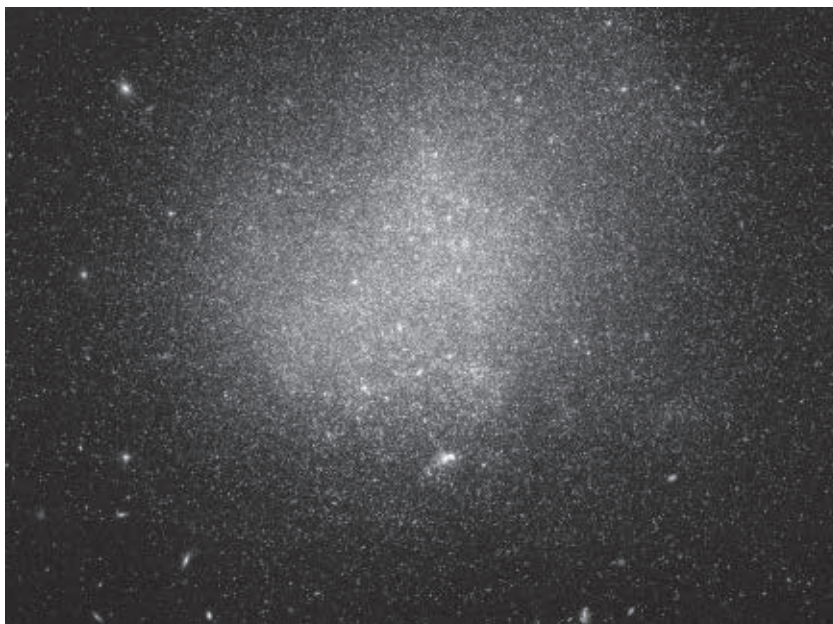


but if there is no finished picture of what the completed puzzle should look like, then you have no clue as to how the pieces *should* be arranged even by colour. Everything is a wild guess.<sup>10</sup>

Take a look at figure 2. Here there are additional ‘bits’. But if they are all unique, there is no common denominator such as geometry or colour to give them some explanation. They just ‘exist’, and that’s all that can be said. You could not even say they are a certain distance apart, because in a random world, how do you identify distance, which is merely a numerical description of how far apart objects are?



**Figure 2.** Unique objects have no relationship to anything else.



**Figure 3.** All the pieces of the universe require an ordered arrangement in order for science to take place.

If you think that a 10,000-piece jigsaw is a challenge, then you can really feel sorry for the unbeliever who has created a nightmare for himself. The universe is not made up of 10,000 pieces but trillions of pieces. In order to ‘make sense’ of any of these pieces, the unbeliever must get at least one piece in its proper place. But how can he do that? He does not even know if a ‘proper place’ exists for any of the pieces. He assumes there is, but he does not make this assumption based on his own worldview. He makes this assumption because Creation is true and he knows no other way to ‘see’ the universe except that somehow the pieces fit together. In other words, the universe is designed (see figure 3).

So what the unbeliever denies with his view of creation, he has to accept when it comes to science. The evolutionary hypothesis requires an unordered universe. But even evolutionary science *assumes* an ordered universe in order to have science. Thus, we truly have schizophrenic man. The idea of man as a *tabula rasa*, a blank slate, is a myth. Not even in Eden could Adam have begun the process of the dominion mandate without the enlightenment he obtained from God as God’s image bearer. So when Adam named the animals, he was not a blank slate guessing at things but already applying the knowledge that God had endowed him within the acts of creation.

But it’s worse than that. The modern scientific method requires neutrality. That means, it requires brute facts—uninterpreted facts. To assume creation is to assume that the facts of the universe are not neutral but are in fact God-ordained facts. That is, all the facts are where they are at the time they are according to the decrees of God. But the scientific method does not permit this assumption. Instead, it requires brute facts—unknowable facts—in order to begin the scientific search for knowledge.

In other words, the modern scientific method requires an irrational beginning to its own process. But from such a starting point, it has nowhere it can go.

## Creed or chaos?

So the unbeliever speaks one thing out of one side of his mouth—the universe is random—while out of the other side of his mouth he demands an ordered universe so that he can have science. Thus it is no coincidence that science arose in the environment of Christianity.<sup>11</sup> In particular, Van Til identifies the key Christian doctrines that make science possible:

“Christianity claims to furnish the presuppositions without which a true scientific procedure is unintelligible. Chief of these presuppositions is the idea of God as expressed in the doctrine of the ontological Trinity. In addition there are the doctrines of creation, of providence, and of God’s ultimate plan with the universe. Christianity claims that the very aim and method of science require these doctrines as their prerequisites.”<sup>12</sup>

Chaos or cosmos? That really is the question. And the unbeliever wants to have it both ways. Enter the law of noncontradiction, which says that A cannot be non-A at the same time and in the same relationship. You cannot be in Sydney and New York at the same time. The universe cannot be ordered and unordered at the same time.

Inherent in the unbeliever’s worldview, then, is a trip between rationality and irrationality. He’s prepared to deny logic in order to maintain his unbelief. And now we begin to see the wisdom of Scripture which says: “Professing to be wise, they became fools.” A fool, according to Proverbs 18:2 is a person who despises knowledge and expresses his own opinion. And that’s the unbeliever. He has opinions about many things but little or no knowledge.<sup>13</sup>

But it is more than cosmos or chaos. It is also a matter of creed or chaos, as Dorothy Sayers so eloquently pointed out:

“We are waging a war of religion. Not a civil war between adherents of the same religion, but a life-and-death struggle between Christian and pagan. ... [A]t bottom, it is a violent and irreconcilable quarrel about the nature of God and nature of man and the ultimate nature of the universe; it is a war of dogma.”<sup>14</sup>

The battle lines have been drawn by those who reject Christian theism. Their dogma, irrational as it is, cannot withstand the light of creation, the Trinity, providence, and rationality that form the essence of Christian dogma. And it is Christian dogma we use to identify that the unbeliever has no clothes. In other words, we show that Christianity “is first and foremost a rational explanation of the universe”.<sup>15</sup>

## Conclusion

If you can just grasp the notion of the jigsaw puzzle, the universe, and trying to find the correct place for any piece

of the puzzle, you are so far ahead in the apologetics game. Certainly far ahead of the unbeliever who really has not the foggiest notion of what you will be talking about. But it is your place to enlighten him, to show him the emperor really has no clothes and is intellectually stark naked.

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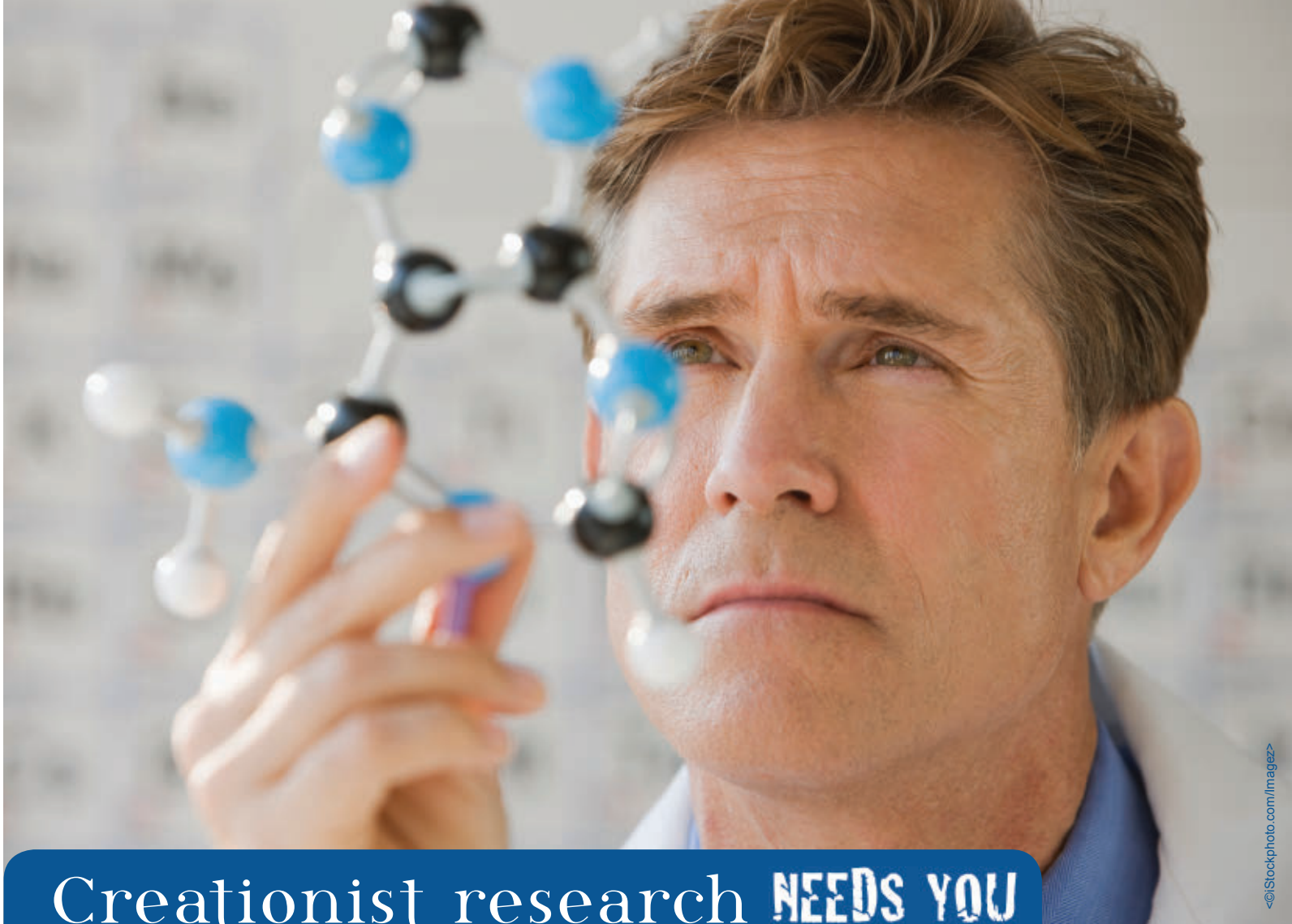
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